

OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:18:36 ; Search time 246.613 Seconds  
 (without alignments)  
 7347.063 Million cell updates/sec

Title: US-09-931-157-1  
 Perfect score: 4105  
 Sequence: 1 gaattcgcgccgcctcttg.....taaaagtttacagaaacctt 4105

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
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 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4105	100.0	4105	4	US-08-121-446-1	Sequence 1, Appli
2	4079	99.4	4079	4	US-09-016-434-1257	Sequence 1257, Ap
3	406.2	9.9	1321	4	US-09-175-658B-20	Sequence 20, Appl
4	395.8	9.6	1470	4	US-09-016-434-1203	Sequence 1203, Ap
5	395.8	9.6	1873	3	US-08-910-864-13	Sequence 13, Appl
6	395.8	9.6	4301	4	US-08-121-446-3	Sequence 3, Appli
7	101.8	2.5	1700	5	PCT-US92-02091-1	Sequence 1, Appli
8	91	2.2	1726	4	US-09-016-434-1215	Sequence 1215, Ap
9	91	2.2	1726	5	PCT-US92-02091-3	Sequence 3, Appli
10	79.6	1.9	1205	3	US-09-120-772-1	Sequence 1, Appli
11	79.6	1.9	1413	4	US-09-016-434-1275	Sequence 1275, Ap

12	68.6	1.7	1352	4	US-09-016-434-1233	Sequence 1233, Ap
13	68.6	1.7	1352	5	PCT-US92-02091-7	Sequence 7, Appli
14	65.8	1.6	1584	5	PCT-US92-02091-5	Sequence 5, Appli
15	63.6	1.5	1563	1	US-08-279-590A-1	Sequence 1, Appli
16	63.6	1.5	1563	1	US-08-910-092-1	Sequence 1, Appli
c 17	51.4	1.3	3095	6	5231168-1	Patent No. 5231168
18	47.4	1.2	1842	4	US-09-170-496D-91	Sequence 91, Appl
19	47.4	1.2	1842	4	US-09-170-496D-211	Sequence 211, App
20	46.8	1.1	1238	4	US-09-761-962A-2	Sequence 2, Appli
21	46.8	1.1	1257	4	US-09-761-962A-5	Sequence 5, Appli
22	46.8	1.1	1334	4	US-09-761-962A-3	Sequence 3, Appli
23	46.8	1.1	1346	4	US-09-761-962A-12	Sequence 12, Appl
24	46.8	1.1	1365	4	US-09-761-962A-11	Sequence 11, Appl
25	46.8	1.1	1423	4	US-09-761-962A-1	Sequence 1, Appli
26	46.8	1.1	1542	4	US-09-761-962A-4	Sequence 4, Appli
27	46.8	1.1	1610	4	US-09-761-962A-16	Sequence 16, Appl
28	46.8	1.1	1729	4	US-09-761-962A-9	Sequence 9, Appli
29	46.8	1.1	1981	3	US-08-387-707-15	Sequence 15, Appl
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33	46	1.1	1164	4	US-09-601-198-65	Sequence 65, Appl
c 34	46	1.1	2563	2	US-08-553-436A-7	Sequence 7, Appli
c 35	45.8	1.1	19124	2	US-08-487-826B-13	Sequence 13, Appl
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37	44.8	1.1	1446	4	US-09-170-496D-81	Sequence 81, Appl
38	44.8	1.1	1446	4	US-09-170-496D-207	Sequence 207, App
39	44.8	1.1	1626	3	US-08-959-381A-4	Sequence 4, Appli
40	44.2	1.1	1610	3	US-08-889-108-7	Sequence 7, Appli
41	44.2	1.1	1610	5	PCT-US94-10358-7	Sequence 7, Appli
42	44.2	1.1	2160	3	US-08-188-275A-1	Sequence 1, Appli
43	44.2	1.1	2162	4	US-09-351-198-1	Sequence 1, Appli
44	44.2	1.1	2162	4	US-09-113-426-1	Sequence 1, Appli
45	44.2	1.1	2162	4	US-09-016-434-1379	Sequence 1379, Ap

#### ALIGNMENTS

#### RESULT 1

US-08-121-446-1

; Sequence 1, Application US/08121446

; Patent No. 6313276

; GENERAL INFORMATION:

; APPLICANT: IMURA, HIROO

; APPLICANT: NAKAO, KAZUWA

; APPLICANT: NAKANISHI, SHIGETADA

; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:



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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 485..1768
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 545
US-08-121-446-1

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Query Match          100.0%; Score 4105; DB 4; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGTCGAGCCCT 120
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Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
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Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
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Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
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Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTTATCGTGGGAATGGTGGGGAATGC	780
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Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
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Db	1141	 TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
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Db	1201	 TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
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Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
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Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
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Db	1741	 GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
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Db	1801	 AATCCTCTCGGAGAAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	 CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040

Db	1981	TTCTGCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
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Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880

Qy	2881	TTCCCTTTTCCATATAGGAAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
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Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCCAAGTGAAGTTTGTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCCAAGTGAAGTTTGTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
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Qy	3301	GTCTGAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720

Qy 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780  
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 Db 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780

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 Db 4081 TAAAATAAAAGTTTACAGAAACCTT 4105

RESULT 2

US-09-016-434-1257

; Sequence 1257, Application US/09016434  
 ; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

```

; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1257:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g219649
US-09-016-434-1257

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Query Match          99.4%; Score 4079; DB 4; Length 4079;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      5 TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGAC 64
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Db      1 TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGAC 60

Qy     65 GGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGTCGAGCCCTCGCG 124
      |||
Db     61 GGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGTCGAGCCCTCGCG 120

Qy    125 CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC 184
      |||
Db    121 CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC 180

Qy    185 CATCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCGGGAGAAGCAG 244
      |||
Db    181 CATCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCGGGAGAAGCAG 240

Qy    245 TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA 304
      |||
Db    241 TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA 300

Qy    305 GCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGC 364
      |||
Db    301 GCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGC 360

Qy    365 CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAA 424
      |||
Db    361 CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAA 420

Qy    425 AGTGAAGGTGTAAAAGCAGCAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG 484
      |||
Db    421 AGTGAAGGTGTAAAAGCAGCAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG 480

Qy    485 ATGGAAACCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 544

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Db	481	 ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	540
Qy	545	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT	604
Db	541	 GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT	600
Qy	605	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	601	 CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	660
Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	724
Db	661	 AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	720
Qy	725	TACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGAATGCAACT	784
Db	721	 TACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGAATGCAACT	780
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	781	 CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	840
Qy	845	AGTCTTGGCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	 AGTCTTGGCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901	 CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961	 TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCCTTTG	1084
Db	1021	 GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCCTTTG	1080
Qy	1085	GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1144
Db	1081	 GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1140
Qy	1145	GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTGTATG	1204
Db	1141	 GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201	 CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	1261	 GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384



Db	1321	GAGATGTTGAAACAGGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGTTGTAATTTTTGCTCTTTGCTGGTTTC	1444
Db	1381	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGTTGTAATTTTTGCTCTTTGCTGGTTTC	1440
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	CCTCTTCACTTAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1564
Db	1501	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1684
Db	1621	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1744
Db	1681	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCCTAGAAGCACTCCTCGGTACTCCCATAATC	1804
Db	1741	AGCCATAAGGACAGCATGAACTGACCACCCCTAGAAGCACTCCTCGGTACTCCCATAATC	1800
Qy	1805	CTCTCGGAGAAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	CTCTCGGAGAAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1924
Db	1861	TTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
Qy	1925	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1984
Db	1921	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTGTGATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	GCGTGTGTGATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2164
Db	2101	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCCCTTCAGCCAAACACAATAT	2224
Db	2161	TAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCCCTTCAGCCAAACACAATAT	2220

Qy	2225	GGGCTCAGGTCAC TTTTATTTGAAATGT CATTTGGTGCCAGTATTTTTTAACTGCATAAT	2284
Db	2221	GGGCTCAGGTCAC TTTTATTTGAAATGT CATTTGGTGCCAGTATTTTTTAACTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATA	2344
Db	2281	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATA	2340
Qy	2345	GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAACAC	2404
Db	2341	GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAACAC	2400
Qy	2405	AAATTCCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
Db	2401	AAATTCCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAAGAACTGTATTTTTATTTTTTAAATGG	2524
Db	2461	GCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAAGAACTGTATTTTTATTTTTTAAATGG	2520
Qy	2525	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCA	2584
Db	2521	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCA	2580
Qy	2585	ATCAGATAGTTCTTTTTTCACAAGTTC AATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2644
Db	2581	ATCAGATAGTTCTTTTTTCACAAGTTC AATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2640
Qy	2645	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCA TTTAACTCTGCCTGAGACTTTTCAG	2704
Db	2641	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCA TTTAACTCTGCCTGAGACTTTTCAG	2700
Qy	2705	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATGA	2764
Db	2701	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATGA	2760
Qy	2765	TTCCGGAATTTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2824
Db	2761	TTCCGGAATTTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2820
Qy	2825	TCCTATTCTCTTAATTTTTTGTTAAAA TGTTAACTGGCAGTAAGTCTTTTTTTGATCATTCC	2884
Db	2821	TCCTATTCTCTTAATTTTTTGTTAAAA TGTTAACTGGCAGTAAGTCTTTTTTTGATCATTCC	2880
Qy	2885	CTTTTCCATATAGGAAACATAATTTTG AAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2944
Db	2881	CTTTTCCATATAGGAAACATAATTTTG AAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2940
Qy	2945	AATAATTACCCACAAAATGCCACCAGTAACTTAACGATTCTTCAC TTTCTTGGGGTTTTTCAG	3004
Db	2941	AATAATTACCCACAAAATGCCACCAGTAACTTAACGATTCTTCAC TTTCTTGGGGTTTTTCAG	3000
Qy	3005	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCCACCATTTCAAAGGGCC	3064
Db	3001	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCCACCATTTCAAAGGGCC	3060

Qy	3065	CACAGTGACTTTTGTCTGGGCATTTTCCCGAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3124
Db	3061	CACAGTGACTTTTGTCTGGGCATTTTCCCGAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3120
Qy	3125	TCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3184
Db	3121	TCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3180
Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
Db	3181	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3240
Qy	3245	TGTATGGATTTAATCTAATCTAATAAATTGTGCCCCGCGAGTTGTGCCAAAGTGCATAGTCT	3304
Db	3241	TGTATGGATTTAATCTAATCTAATAAATTGTGCCCCGCGAGTTGTGCCAAAGTGCATAGTCT	3300
Qy	3305	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3364
Db	3301	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3360
Qy	3365	GCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3424
Db	3361	GCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480
Qy	3485	TTGATAAAGCAGTATTTGGGGTTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3544
Db	3481	TTGATAAAGCAGTATTTGGGGTTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3540
Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
Db	3541	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3600
Qy	3605	TGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3664
Db	3601	TGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3660
Qy	3665	GTTGGGGCCATATTTTAGGACAGGTAAAAAATCATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGGCCATATTTTAGGACAGGTAAAAAATCATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTTCACACCATTTTGTTTAGACAA	3844
Db	3781	ATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTTCACACCATTTTGTTTAGACAA	3840
Qy	3845	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTC	3904
Db	3841	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTC	3900
Qy	3905	AGAAAGTCATAGATTTTCTGAAGGCGTCAACGTGCATTTTATTATTAGGACTGGTAAGTAAC	3964

Db	3901	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3960
Qy	3965	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4024
Db	3961	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4020
Qy	4025	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA	4083
Db	4021	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA	4079

### RESULT 3

US-09-175-658B-20

; Sequence 20, Application US/09175658B

; Patent No. 6372900

; GENERAL INFORMATION:

; APPLICANT: METALLINOS, DANIKA

APPLICANT: RINE, JASPER

; APPLICANT: BOWLING, ANN

; TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS

; FILE REFERENCE: GOBR-110

; CURRENT APPLICATION NUMBER: US/09/175,658B

; CURRENT FILING DATE: 1998-10-20

; PRIOR APPLICATION NUMBER: 60/062,562

; PRIOR FILING DATE: 1997-10-21

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; NUMBER OF SEQ ID NOS: 25
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; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 20

; LENGTH: 1321

; TYPE: DNA

; ORGANISM: Horse

US-09-175-658B-20

Query Match 9.9%; Score 406.2; DB 4; Length 1321;

Best Local Similarity 67.2%; Pred. No. 1.8e-95:

Matches 630; Conservative 0; Mismatches 283; Indels 24; Gaps 3;

Qy 717 CTTTCAAATACATTAACTGTGATATCTTGTA CTATTTTCATCGTGGGAATGGTGGGGA 776

Db 310 CTTTCAAGTACATCAACACAGTAGTGTCCTGCCTAGTGTTCTGTGCTGGGCATCATCGGAA 369

Qy 777 ATGCAACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGC 836

Db 370 ACTCCACACTGCTGAGAATCATTACAGAACAAGTGCATGCGGAACGGCCCTAATATCT 429

Qy 837 TGATAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATG 896

Db 430 TGATCGCCAGCCTGGCTCTCCGAGACCTGCTGCAAATCATCATTGACGTCCCATCAATG 489

Qy 897 TATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTT 956

Db 490 TCTACAAGCTGCTGGCTGAGGACTGGCC-----CTTTGGAGTCGAGATGT 534

Qy 957 GCAAGCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCG 1016

Db 535 GTAAGCTGGTGCCTTTCATACAGAAGGCCTCCGTGGGCATCACTGTGCTGAGTCTGTGTG 594

Qy 1017 CTCTTAGTGTGGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTT CAGGGAATTGGGA 1076  
 |||| ||| ||||| || |||| ||||| |||| | || ||| ||||| ||  
 Db 595 CTCTAAGTATTGACAGATATCGAGCTGTTGCTTCCTTGGAGCGAATTAAAGGAATTCGGG 654

Qy 1077 TTCCTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCA 1136  
 |||| || ||| ||||| || |||| | || ||| ||||| ||  
 Db 655 TTCCAAAATGGACAGCAGTAGAAATTGTTTAAATTGGGTGGTCTCTGTGGTTCTGGCTG 714

Qy 1137 TTCCTGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAA 1196  
 | ||||| || || ||| || || || || || || || || || || || ||  
 Db 715 TCCCTGAAGCCGTGGGTTTTGATATGATTACCGCTGACTACAAAGGAAGTTATCTGCGAA 774

Qy 1197 CCTGTATGCTCAATGCCAC-----ATCAAAATTCATGGAGTTCTACCAAGATGTAAAGG 1250  
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 Db 775 TCTGCCTGCTTCATCCCACTCAGAAAACAGCCTTCATGCAGTTTACAAGAATGCTAAGG 834

Qy 1251 ACTGGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACA 1310  
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 Db 835 ACTGGTGGCTATTTAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATA 894

Qy 1311 CCCTCATGACTTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTG 1370  
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 Db 895 CCTTGATGACCTGTGAAATGTTGAGAAAGAAGAGTGGCA--TGCAAATTGCTTTAAATG 951

Qy 1371 AACATCTTAAGCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTG 1430  
 | || | ||||| || | ||||| ||||| ||||| ||||| |||| | || ||||  
 Db 952 ATCACTTAAAGCAGAGAAGGGAAGTGGCGAAAACAGTATTCTGCCTGGTCTTGTCTTTG 1011

Qy 1431 CTCTTTGCTGGTTCCCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAAA 1490  
 | || ||||| || ||||| || || || || || || || || || || || ||  
 Db 1012 CCCTGTGCTGGCTTCCTCTTCACCTCAGCAGGATTTTGAAACACACTCTTTATGATCAGA 1071

Qy 1491 TGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTA 1550  
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 Db 1072 ATGATCCCATAGATGTGAACCTTTTGAGCTTTTGTGGTATTGGACTACATTGGCATCA 1131

Qy 1551 ACTTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAAT 1610  
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 Db 1132 ACATGGCCTCCCTGAATTCCTGCATTAATCCAATAGCTCTGTATTTGGTGAGCAAAGAT 1191

Qy 1611 TTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGCTG 1647  
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 Db 1192 TCAAAAACCTGCTTTAAGTCGTGCTTATGCTGCTGGTG 1228

#### RESULT 4

US-09-016-434-1203

; Sequence 1203, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1203:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1470 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g182275
US-09-016-434-1203

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Query Match          9.6%; Score 395.8; DB 4; Length 1470;
Best Local Similarity 65.7%; Pred. No. 9.7e-93;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
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Db      314 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 373

Qy      749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
        | | ||| |  |||| |  |  |||| |  |  |||| |  |  |||| |  |  |||| |
Db      374 CTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 433

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 868
        || |  ||| |  || |  |||| |  |||| |  || |  |||| |  || |  |||| |
Db      434 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 493

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
        |  |  |||| |  |||| |  |||| |  |||| |  |||| |  || |  |||| |
Db      494 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 549

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Qy	929	GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTCGAGAAGTCCTCG	988
Db	550	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	598
Qy	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC	1048
Db	599	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	658
Qy	1049	TCCTGGAGTCGTGTTTCAAGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Db	659	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	718
Qy	1109	ATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAAGCGATTGGCTTCGTTCATGGTACCC	1168
Db	719	ATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	778
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	779	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAAGACAGCT	838
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTTATTTCTGTATG	1282
Db	839	TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTTG	898
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	899	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAG	955
Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	956	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1015
Qy	1403	ACAGTTTTTCTGCTTGGTTGTAATTTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT	1462
Db	1016	ACCGTCTTTTGCTTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACTCAGCAGG	1075
Qy	1463	ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1076	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTT	1135
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAACCTTGGCAACCATGAATTCATGTATAAACCCC	1582
Db	1136	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1195
Qy	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1642
Db	1196	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC	1255
Qy	1643	TGCTG 1647	
Db	1256	TGGTG 1260	

RESULT 5

US-08-910-864-13

; Sequence 13, Application US/08910864

; Patent No. 6280931

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; GENERAL INFORMATION:
;   APPLICANT:  SAKAMOTO, AIJI
;   APPLICANT:  HANAOKA, FUMIO
;   TITLE OF INVENTION:  METHOD FOR SPECIFICALLY AMPLIFYING A cDNA OF AN
EXTREMELY
;   TITLE OF INVENTION:  SMALL QUANTITY
;   NUMBER OF SEQUENCES:  13
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  FISH & RICHARDSON P.C.
;     STREET:    4225 EXECUTIVE SQUARE, SUITE 1400
;     CITY:      LA JOLLA
;     STATE:     CA
;     COUNTRY:   USA
;     ZIP:       92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/910,864
;     FILING DATE:       13-AUG-1997
;     CLASSIFICATION:    435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 216506/1996
;     FILING DATE:       16-AUG-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  HAILE, LISA A.
;     REGISTRATION NUMBER:  38,347
;     REFERENCE/DOCKET NUMBER:  07898/017001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  619-678-5070
;     TELEFAX:    619-678-5099
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1873 base pairs
;       TYPE:    nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  231..1556
US-08-910-864-13

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Query Match          9.6%;  Score 395.8;  DB 3;  Length 1873;
Best Local Similarity 65.7%;  Pred. No. 1.1e-92;
Matches 634;  Conservative 0;  Mismatches 307;  Indels 24;  Gaps 3;

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Qy      689  TGCCACAGCAGACTAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
          |||| | | | | | | | | | | | | | | | | | | | |
Db      498  TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 557

Qy      749  ACTATTTTCATCGTGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
          | | ||| | | ||| | | |||| | | | | | | | | | |
Db      558  CTTGTGTTCTGCTGCGGGATCATCGGGAATCCACACTTCTGAGAATTATCTACAAGAAC 617

```



Qy	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC	868
Db	618	AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	677
Qy	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Db	678	CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	733
Qy	929	GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCGAGAAGTCTCTCG	988
Db	734	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	782
Qy	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC	1048
Db	783	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	842
Qy	1049	TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Db	843	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGTTTTG	902
Qy	1109	ATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCC	1168
Db	903	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	962
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	963	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT	1022
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG	1282
Db	1023	TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTATTCAGTTTCTATTTCTGCTTG	1082
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	1083	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAG	1139
Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1140	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1199
Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT	1462
Db	1200	ACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTACCTCAGCAGG	1259
Qy	1463	ATATTGAAGAAAACGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1260	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTGAGCTTT	1319
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC	1582
Db	1320	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1379
Qy	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATGTTTCCAGTCATGCCTCTGCTGC	1642
Db	1380	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAACTGCTTTAAGTCATGCTTATGCTGC	1439
Qy	1643	TGCTG	1647

Db            || ||  
             1440 TGGTG 1444

RESULT 6

US-08-121-446-3

; Sequence 3, Application US/08121446  
; Patent No. 6313276  
; GENERAL INFORMATION:  
; APPLICANT: IMURA, HIROO  
; APPLICANT: NAKAO, KAZUWA  
; APPLICANT: NAKANISHI, SHIGETADA  
; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/121,446  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/911,684  
; FILING DATE: 10-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CIOTTI, THOMAS E.  
; REGISTRATION NUMBER: 21,013  
; REFERENCE/DOCKET NUMBER: 29900-20324.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4301 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 238..1566

US-08-121-446-3

Query Match                    9.6%;   Score 395.8;   DB 4;   Length 4301;  
Best Local Similarity       65.7%;   Pred. No. 1.7e-92;  
Matches 634;   Conservative       0;   Mismatches 307;   Indels    24;   Gaps       3;

Qy            689 TGCCACAGCAGACTAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Db	505	TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC	564
Qy	749	ACTATTTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC	808
Db	565	CTTGTGTTCGTGCTGGGGATCATCGGGAACCCACACTTCTGAGAATTATCTACAAGAAC	624
Qy	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC	868
Db	625	AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	684
Qy	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Db	685	CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	740
Qy	929	GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTGCAGAAGTCCTCG	988
Db	741	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	789
Qy	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC	1048
Db	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Qy	1049	TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Db	850	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Qy	1109	ATCTGGATCCTGTCCTTTATCCTGGCCATTCTTGAAGCGATTGGCTTCGTCATGGTACCC	1168
Db	910	ATTTGGGTGGTCTCTGTGGTTCGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT	1029
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTATTTTCTGTATG	1282
Db	1030	TTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG	1089
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAG	1146
Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1147	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1206
Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT	1462
Db	1207	ACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGG	1266
Qy	1463	ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1267	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT	1326
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAACCTTGGCAACCATGAATTCATGTATAAACCCC	1582

Db           1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGCATTAAACCCA 1386

QY           1583 ATAGCTCTGTATTTTG TGAGCAAGAAAATTTAAAAAATTGTTTCAGTCATGCCTCTGCTGC 1642  
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Db           1387 ATTGCTCTGTATTTGGTGAGCAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGC 1446

QY           1643 TGCTG 1647  
    || |

Db           1447 TGGTG 1451

PCT-US92-02091-1

; GENERAL INFORMATION:

APPLICANT: Corjay, Martha H.

APPLICANT: Harkins, Richard N.

NUMBER OF SEQUENCES: 8

ADDRESSEE: Edwin P. Ching

CITY: Alameda

COUNTRY: USA

; COMPUTER READ.

COMPUTER: IBM PC compatible

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; SOFTWARE: PatentIn Release #1.0

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APPLICATION NUMBER: PC

CLASSIFICATION: 435

APPLICATION NUMBER: US 07/426,150

; PRIOR APPLICATION DATA:

; FILING DATE: 05-JUN-1990

; NAME: Ching, Edwin P.

REFERENCE/DOCKET NUMBER: A-0092C

; TELEPHONE: 415-266-7476

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; INFORMATION FOR SEQ ID NO: 1:
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;      LENGTH:  1700 base pairs
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; STRANDEDNESS: double
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; MOLECULE TYPE: cDNA to mRNA

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;   HYPOTHETICAL:  NO
;   ORIGINAL SOURCE:
;   ORGANISM:  Mus musculus
;   CELL LINE:  Swiss 3T3
;   IMMEDIATE SOURCE:
;   LIBRARY:  Lambda GT10
;   FEATURE:
;   NAME/KEY:  CDS
;   LOCATION:  378..1532
PCT-US92-02091-1

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Query Match          2.5%;  Score 101.8;  DB 5;  Length 1700;
Best Local Similarity 49.3%;  Pred. No. 2.1e-16;
Matches 308;  Conservative 0;  Mismatches 302;  Indels 15;  Gaps 1;

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Qy      714 CAGCTTTCAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGAATGGTGG 773
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      490 CGGGCTTCATCTATGTCATCCCTGCAGTTTATGGGCTTATCATCGTGATAGGTCTTATTG 549

Qy      774 GGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACG 833
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      550 GCAACATCAGCTCATCAAGATCTTCTGCACGGTCAAGTCCATGCGAAACGTGCCAAACC 609

Qy      834 CGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCA 893
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      610 TGTTTCATCTCTAGCCTGGCTTTGGGAGACCTGCTGCTGCTGGTGACATGCGCCCCTGTGG 669

Qy      894 ATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTTC 953
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      670 ATGCCAGCAAGTACCTGGCTGACAGGTGGCTA-----TTTGGCAGAATTG 714

Qy      954 TTTGCAAGCTGTTCCCTTTTTTGCAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCT 1013
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      715 GCTGCAAACTGATCCCCTTTATACAACTTACTTCAGTGGGGGTGTCTGTCTTCACACTTA 774

Qy      1014 GCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTG 1073
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      775 CGGCACTGTGCTGACAGGTACAAAGCCATTGTACGGCCAATGGATATCCAGGCATCCC 834

Qy      1074 GGATTCCTTTGGTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGG 1133
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      835 ATGCCCTGATGAAGATCTGTCTCAAAGCTGCTTTGATCTGGATTGTCTCTATGTTGTTGG 894

Qy      1134 CCATTCCTGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATA 1193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      895 CCATCCCAGAGGCTGTGTTTTCTGACCTCCACCCCTTCCATGTGAAAGATACCAACCAAA 954

Qy      1194 AAACCTGTATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACT 1253
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      955 CCTTCATTAGTTGTGCCCCCTACCCACACTCCAATGAGCTACACCCTAAAATCCATTCCA 1014

Qy      1254 GGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCC 1313
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1015 TGGCTTCCTTTCTGGTTTTCTACGTTATCCCACTGGCGATCATCTCTGTCTACTACTACT 1074

Qy      1314 TCATGACTTGTGAGATGTTGAACAG 1338
      | | | | | | | | | | | | | | | | | |

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Db 1075 TCATTGCCCCGAAATCTGATTGAG 1099

RESULT 8

US-09-016-434-1215

; Sequence 1215, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1215:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1726 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK

; CLONE: g183649

US-09-016-434-1215

Query Match 2.2%; Score 91; DB 4; Length 1726;

Best Local Similarity 48.3%; Pred. No. 1.3e-13;

Matches 299; Conservative 0; Mismatches 305; Indels 15; Gaps 1;

Qy 720 TCAAATACATTAACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATG 779  
|| || | | || | | | || | | | || | | | ||

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Db      514 TCCTCTATGTCATCCCTGCAGTTTATGGGGTTATCATTCTGATAGGCCTCATTGGCAACA 573
Qy      780 CAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGA 839
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      574 TCACCTTGATCAAGATCTTCTGTACAGTCAAGTCCATGCGAAACGTTCCAAACCTGTTCA 633
Qy      840 TAGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTAT 899
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      634 TTTCCAGTCTGGCTTTGGGAGACCTGCTCCTCCTAATAACGTGTGCTCCAGTGGATGCCA 693
Qy      900 TTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCA 959
      | | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      694 GCAGGTACCTGGCTGACAGATGGCTATTTGGCAGGATTGGC-----TGCA 738
Qy      960 AGCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTC 1019
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      739 AACTGATCCCTTTTATACAGCTTACCTCTGTTGGGGTGTCTGTCTTCACACTCACGGCGC 798
Qy      1020 TTAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTC 1079
      | | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      799 TCTCGGCAGACAGATACAAAGCCATTGTCCGGCCAATGGATATCCAGGCCTCCCATGCCC 858
Qy      1080 CTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTC 1139
      || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      859 TGATGAAGATCTGCCTCAAAGCCGCCTTTATCTGGATCATCTCCATGCTGCTGGCCATTC 918
Qy      1140 CTGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCT 1199
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      919 CAGAGGCCGTGTTTTCTGACCTCCATCCCTTCCATGAGGAAAGCACCAACCAGACCTTCA 978
Qy      1200 GTATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGC 1259
      || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      979 TTAGCTGTGCCCCATACCCACACTCTAATGAGCTTCACCCCAAATCCATTCTATGGCTT 1038
Qy      1260 TCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGA 1319
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1039 CCTTTCTGGTCTTCTACGTCATCCCACTGTGATCATCTCTGTTTACTACTACTTCATTG 1098
Qy      1320 CTTGTGAGATGTTGAACAG 1338
      || | ||| ||| ||| |||
Db      1099 CTAAAAATCTGATCCAGAG 1117

```

RESULT 9

PCT-US92-02091-3

; Sequence 3, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

```

; STATE: CA
; COUNTRY: USA
; ZIP: 94501
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02091
; FILING DATE: 19920313
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/426,150
; FILING DATE: 24-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/533,659
; FILING DATE: 05-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34090
; REFERENCE/DOCKET NUMBER: A-0092C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-266-7476
; TELEFAX: 415-266-7400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1726 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Small cell lung carcinoma
; CELL LINE: NCI-H345
; IMMEDIATE SOURCE:
; LIBRARY: Lambda GT10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 399..1553
PCT-US92-02091-3

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Query Match          2.2%; Score 91; DB 5; Length 1726;
Best Local Similarity 48.3%; Pred. No. 1.3e-13;
Matches 299; Conservative 0; Mismatches 305; Indels 15; Gaps 1;

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Qy      720 TCAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATG 779
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      514 TCCTCTATGTCATCCCTGCAGTTTATGGGGTTATCATTCTGATAGGCCTCATTGGCAACA 573

Qy      780 CAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGA 839
          ||| || ||| |||| ||  ||  ||| ||  ||  ||  ||  ||  ||
Db      574 TCACTTTGATCAAGATCTTCTGTACAGTCAAGTCCATGCGAAACGTTCCAAACCTGTTCA 633

Qy      840 TAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTAT 899

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      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      634 TTTCCAGTCTGGCTTTGGGAGACCTGCTCCTCCTAATAACGTGTGCTCCAGTGGATGCCA 693
Qy      900 TTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCA 959
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      694 GCAGGTACCTGGCTGACAGATGGCTATTTGGCAGGATTGGC-----TGCA 738
Qy      960 AGCTGTTCCCTTTTTGCGAAGTCCTCGGTGGGGATCACCGTCTCAACCTCTGCGCTC 1019
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      739 AACTGATCCCTTTTATACAGCTTACCTCTGTTGGGGTGTCTGTCTTCACACTCACGGCGC 798
Qy     1020 TTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTACAGGAATTGGGATTC 1079
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      799 TCTCGGCAGACAGATACAAAGCCATTGTCCGGCCAATGGATATCCAGGCCTCCCATGCCC 858
Qy     1080 CTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTC 1139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      859 TGATGAAGATCTGCCTCAAAGCCGCCTTTATCTGGATCATCTCCATGCTGCTGGCCATTC 918
Qy     1140 CTGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCT 1199
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      919 CAGAGGCCGTGTTTTCTGACCTCCATCCCTTCCATGAGGAAAGCACCAACCAGACCTTCA 978
Qy     1200 GTATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGC 1259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      979 TTAGCTGTGCCCCATACCCCACTCTAATGAGCTTCACCCCAAATCCATTCTATGGCTT 1038
Qy     1260 TCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGA 1319
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1039 CCTTTCTGGTCTTCTACGTCACTCCACTGTGATCATCTCTGTTTACTACTACTTCATTG 1098
Qy     1320 CTTGTGAGATGTTGAACAG 1338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1099 CTAAAAATCTGATCCAGAG 1117

```

RESULT 10

US-09-120-772-1

; Sequence 1, Application US/09120772

; Patent No. 6143521

; GENERAL INFORMATION:

; APPLICANT: LANE, PAMELA

; APPLICANT: TSUI, PING

; APPLICANT: ELSHOURBAGY, NABIL

; TITLE OF INVENTION: HUMAN BOMBESIN RECEPTOR SUBTYPE

; TITLE OF INVENTION: 3

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ratner & Prestia

; STREET: P.O. Box 980

; CITY: Valley Forge

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

```

;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/120,772
;      FILING DATE:  22-JUL-1998
;      CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Prestia, Paul F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GP-70505
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0700
;      TELEX:  846169
;      INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  1205 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  cDNA
US-09-120-772-1

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Query Match          1.9%;  Score 79.6;  DB 3;  Length 1205;
Best Local Similarity  46.9%;  Pred. No. 9.9e-11;
Matches  419;  Conservative  0;  Mismatches  439;  Indels  36;  Gaps  4;

```

```

Qy      761 GTGGGAATGGTGGGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGG 820
      ||||| || | || ||||| || | || || || || || || || || ||
Db      180 GTGGGCATCCTTGGAATGCTATTCTCATCAAAGTCTTTTTCAAGACCAAATCCATGCAA 239

Qy      821 AATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATT 880
      | | | || | | | | | | | | | | | | | | | | | | | | | |
Db      240 ACAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACT 299

Qy      881 GATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGAC 940
      | | || | | || | | | | | | | | | | | | | | | |
Db      300 TGTGTGCCAGTGGATGCAACTCACTACCTTGCAAGGATGGCTGTTC----- 347

Qy      941 TTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACC 1000
      || | | | | | | | | | | | | | | | | | | | | | |
Db      348 ---GGAAGAATTGGTTGTAAGTGCTCTCTTTTCATCCGGCTCACTTCTGTTGGTGTGTCA 404

Qy      1001 GTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGT 1060
      || ||| | | || | | | | | | | | | | | | | | |
Db      405 GTGTTACATTAGCAATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAG 464

Qy      1061 GTTCAGGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTG 1120
      ||| | | | | | | | | | | | | | | | | | | | |
Db      465 CGACAGCCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTG 524

Qy      1121 TCCTTTATCCTGGCCATTTCCTGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGG 1180
      || | | | | | | | | | | | | | | | | | | | | |
Db      525 TCTATGATATTTGCTCTACCTGAGGCTATATTTTCAAATGTATACACTTTTCGAGATCCC 584

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Qy 1181 GGTGAACAGCATAAACCTGTATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAA 1240  
 | | | | | | | | | | | | | | | | | |  
 Db 585 AATAAAAATATGACATTTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAA 644

Qy 1241 GATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCG 1300  
 | | | | | | | | | | | | | | | | | |  
 Db 645 GAAATACATTCTCTGCTGTGCTTCTTAGTGTTCTACATTATTCCACTCTCTATTATCTCT 704

Qy 1301 ATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATT 1360  
 | | | | | | | | | | | | | | | | | |  
 Db 705 GTCTACTATTCTTGATTGCTAGGACCCTTTACAAAAGCACCTGAACATACCTACTGAG 764

Qy 1361 GCCCTCAGTGAACATCTTAAGCAG-----CGTCGAGAAGTGGCAAAAACAGTTTTTC 1411  
 | | | | | | | | | | | | | | | | | |  
 Db 765 GAACAAAGCCATGCCCGTAAGCAGATTGAATCCCGAAAGAGAATTGCCGAAACGGTATTG 824

Qy 1412 TGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGTATATTGAAG 1471  
 | | | | | | | | | | | | | | | | | |  
 Db 825 GTGTTGGTGGCTCTGTTTGGCCTCTGCTGGTTGCCAAATCACCT--CCTGTACCTCTACC 882

Qy 1472 AAAACTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTC 1531  
 | | | | | | | | | | | | | | | | | |  
 Db 883 ATTCATTCACTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTTCATTTTACCATT- 941

Qy 1532 ATGGATTACATCGGTATTAAGTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTG 1591  
 | | | | | | | | | | | | | | | | | |  
 Db 942 -----TTCTCTCGGGTTTTGGCTTTTCAGCAATTCTTGCGTAAACCCCTTTGCTCTC 992

Qy 1592 TATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGC 1645  
 | | | | | | | | | | | | | | | | | |  
 Db 993 TACTGGCTGAGCAAAAGCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTGC 1046

RESULT 11

US-09-016-434-1275

; Sequence 1275, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:



Qy 1181 GGTGAACAGCATAAAACCTGTATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAA 1240  
 | | | | | | | | | | | | | | | | | |  
 Db 732 AATAAAAATATGACATTTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAA 791

Qy 1241 GATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCG 1300  
 | | | | | | | | | | | | | | | | | |  
 Db 792 GAAATACATTCTCTGCTGTGCTTCTTAGTGTTCTACATTATTCCACTCTCTATTATCTCT 851

Qy 1301 ATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATT 1360  
 | | | | | | | | | | | | | | | | | |  
 Db 852 GTCTACTATTCTTGATTGCTAGGACCCCTTTACAAAAGCACCTGAACATACCTACTGAG 911

Qy 1361 GCCCTCAGTGAACATCTTAAGCAG-----CGTCGAGAAGTGGCAAAAACAGTTTTTC 1411  
 | | | | | | | | | | | | | | | | | |  
 Db 912 GAACAAAGCCATGCCCGTAAGCAGATTGAATCCCGAAAGAGAATTGCCGAAACGGTATTG 971

Qy 1412 TGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGTATATTGAAG 1471  
 | | | | | | | | | | | | | | | | | |  
 Db 972 GTGTTGGTGGCTCTGTTTGCCCTCTGCTGGTTGCCAAATCACCT--CCTGTACCTCTACC 1029

Qy 1472 AAAACTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTC 1531  
 | | | | | | | | | | | | | | | | | |  
 Db 1030 ATTCATTCACTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTTCACTTTTACCATT- 1088

Qy 1532 ATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTG 1591  
 | | | | | | | | | | | | | | | | | |  
 Db 1089 -----TTCTCTCGGGTTTGGCTTTCAGCAATTCTTGCGTAAACCCCTTTGCTCTC 1139

Qy 1592 TATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGC 1645  
 | | | | | | | | | | | | | | | | | |  
 Db 1140 TACTGGCTGAGCAAAAGCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTGC 1193

RESULT 12

US-09-016-434-1233

; Sequence 1233, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434



```

RESULT 13
PCT-US92-02091-7
; Sequence 7, Application PC/TUS9202091
; GENERAL INFORMATION:
;   APPLICANT:  Battey Jr., James F.
;   APPLICANT:  Corjay, Martha H.
;   APPLICANT:  Feldman, Richard I.
;   APPLICANT:  Harkins, Richard N.
;   TITLE OF INVENTION:  RECEPTORS FOR BOMBESIN-LIKE PEPTIDES
;   NUMBER OF SEQUENCES:  8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Edwin P. Ching
;     STREET:    1501 Harbor Bay Parkway
;     CITY:      Alameda
;     STATE:     CA
;     COUNTRY:   USA
;     ZIP:       94501
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US92/02091
;     FILING DATE:        19920313
;     CLASSIFICATION:     435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/426,150
;     FILING DATE:        24-OCT-1989
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/533,659
;     FILING DATE:        05-JUN-1990
;   ATTORNEY/AGENT INFORMATION:
;     NAME:              Ching, Edwin P.
;     REGISTRATION NUMBER:  34090
;     REFERENCE/DOCKET NUMBER:  A-0092C
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:         415-266-7476
;     TELEFAX:           415-266-7400
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:          1352 base pairs
;       TYPE:             NUCLEIC ACID
;       STRANDEDNESS:     double
;       TOPOLOGY:         linear
;     MOLECULE TYPE:      cDNA to mRNA
;     HYPOTHETICAL:      NO
;     ORIGINAL SOURCE:
;       ORGANISM:         Homo sapiens
;       CELL TYPE:        Small cell lung carcinoma
;       CELL LINE:        NCI-H345
;     FEATURE:
;       NAME/KEY:         CDS
;       LOCATION:         140..1312
PCT-US92-02091-7

Query Match                1.7%;  Score 68.6;  DB 5;  Length 1352;

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Best Local Similarity 50.1%; Pred. No. 7.6e-08;  
Matches 210; Conservative 0; Mismatches 194; Indels 15; Gaps 1;

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Qy      752 ATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAACAA 811
      || ||| ||||| || ||||| || ||| || ||||| || ||| |||
Db      296 ATCATCACCGTGGGCTTGCTGGGCAACATCATGCTGGTGAAGATCTTCATCACCAACAGC 355

Qy      812 TGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTAT 871
      ||||| || ||||| || || || || || || || || || ||
Db      356 GCCATGAGGAGCGTCCCCAACATCTTCATCTCTAACCTGGCGGCCGGGACTTGCTGCTG 415

Qy      872 GTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGAT 931
      || ||| || ||| || || || || || || || || || || ||
Db      416 CTGCTCACCTGCGTCCC-----GGTGGACGCCTCGCGCTACTTCTTCGAC 460

Qy      932 CACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAGTCCTCGGTG 991
      | ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db      461 GAGTGGATGTTTGGCAAGGTGGGCTGCAAACTGATCCCTGTCATCCAGCTCACTTCCGTG 520

Qy      992 GGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCC 1051
      ||| | |||| ||| ||| || || || || || || || || || || || || || ||
Db      521 GGGGTTTCCGTGTTCACTCTCACTGCCCTCAGCGCCGACAGGTACAGAGCCATCGTTAAC 580

Qy      1052 TGGAGTCGTGTTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCCATC 1111
      | || || ||| ||| || || || || || || || || || || || || || || ||
Db      581 CCCATGGACATGCAGACGTGAGGGGCATTGCTGCGGACCTGTGTGAAGGCCATGGGTATC 640

Qy      1112 TGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTTCATGGTACCCTT 1170
      ||| | ||| | ||||| ||||| ||||| || || || || || || || || || || ||
Db      641 TGGGTGGTCTCCGTGTTGCTGGCAGTTCCCGAAGCGGTGTTTTTCAGAAGTGGCTCGCAT 699
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RESULT 14

PCT-US92-02091-5

; Sequence 5, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

; STATE: CA

; COUNTRY: USA

; ZIP: 94501

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/02091

; FILING DATE: 19920313



```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/426,150
; FILING DATE: 24-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/533,659
; FILING DATE: 05-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34090
; REFERENCE/DOCKET NUMBER: A-0092C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-266-7476
; TELEFAX: 415-266-7400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1584 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; TISSUE TYPE: Esophagus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 132..1304
PCT-US92-02091-5

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Query Match          1.6%; Score 65.8; DB 5; Length 1584;
Best Local Similarity 49.6%; Pred. No. 4.4e-07;
Matches 209; Conservative 0; Mismatches 197; Indels 15; Gaps 1;

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Qy      752 ATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTCACAGAACAAA 811
      || || |||| || |||| || | ||| | ||| | ||| | |||
Db      288 ATCATCTCGGTGGGCTTGCTGGGCAACATCATGCTGGTGAAGATATTCCTCACCAACAGC 347

Qy      812 TGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTAT 871
      ||| ||| || ||||| || || | || | ||| ||| ||| |||
Db      348 ACCATGCGGAGTGTCCCCAACATCTTCATCTCTAACCTGGCTGCGGGAGACCTGCTGCTG 407

Qy      872 GTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGAT 931
      || | | |||| | ||| | || | ||| ||| ||| ||| |||
Db      408 CTGCTGACCTGCGTCCCAGTGGATGCCTCC-----CGATACTTCTTTGAT 452

Qy      932 CACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCGAGAAGTCCTCGGTG 991
      | | | ||| || |||| || ||| || ||| ||| ||| ||| |||
Db      453 GAATGGGTGTTTCGGCAAGCTGGGCTGCAAACATCCCAGCCATCCAGCTCACCTCGGTG 512

Qy      992 GGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCC 1051
      ||| | |||| || ||| || ||| ||| ||| ||| ||| ||| |||
Db      513 GGGGTTTCCGTGTTCACTCTACGGCCCTCAGCGCTGACAGGTACAGAGCTATCGTGAAC 572

Qy      1052 TGGAGTCGTGTTCAGGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCCATC 1111
      | | | ||| ||| | || | || | || | || | ||| ||| |||
Db      573 CCCATGGACATGCAGACGTCCTGGTGTGGTGCTGTGGACCAGTTTGAAGGCCGTGGGCATC 632

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Qy      1112 TGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCCTTT 1171
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Db      633 TGGGTGGTCTCTGTGCTGTTGGCTGTCCCTGAGGCTGTGTTTTCGGAAGTAGCACGCATC 692

Qy      1172 G 1172
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RESULT 15

US-08-279-590A-1

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; Sequence 1, Application US/08279590A
; Patent No. 5656749
; GENERAL INFORMATION:
;   APPLICANT: ELIOT R. SPINDEL, SRINIVASA
;   APPLICANT: NAGALLA AND BRENDA BARRY
;   TITLE OF INVENTION: NUCLEIC ACIDS ENCODING
;   TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE
;   TITLE OF INVENTION: PEPTIDES
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: U.S.A.
;     ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;     COMPUTER: IBM PS/2 Model 50Z or 55SX
;     OPERATING SYSTEM: MS-DOS (Version 5.0)
;     SOFTWARE: WordPerfect (Version 5.1)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/279,590A
;     FILING DATE: July 22, 1994
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: No. 5656749e
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Y. Rocky Tsao
;     REGISTRATION NUMBER: 34,053
;     REFERENCE/DOCKET NUMBER: 00537/098001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617) 542-5070
;     TELEFAX: (617) 542-8906
;     TELEX: 200154
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1563
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear

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US-08-279-590A-1

Query Match 1.5%; Score 63.6; DB 1; Length 1563;

Best Local Similarity 45.5%; Pred. No. 1.6e-06;  
Matches 332; Conservative 0; Mismatches 374; Indels 24; Gaps 2;

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Qy      735 CTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGA 794
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Db      985 GCAAACGAGTGGCAAAAACAGTTTCTGCTTGGTGTGGTGGCATTGTTGCGAGTGTGCTGGTTGC 1044

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Db      1045 CAAACCACAT 1054

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Job time : 254.613 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 10:54:32 ; Search time 1202.3 Seconds  
(without alignments)  
11347.756 Million cell updates/sec

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Perfect score: 4105  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
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1	4105	100.0	4105	9	US-09-931-157-1	Sequence 1, Appli
2	4105	100.0	4105	13	US-10-007-926A-229	Sequence 229, App
3	4105	100.0	4105	13	US-10-101-510-370	Sequence 370, App
4	4105	100.0	4105	15	US-10-225-567A-115	Sequence 115, App
5	2470	60.2	2595	10	US-09-919-497-12	Sequence 12, Appl
6	2470	60.2	2595	13	US-10-204-752-30	Sequence 30, Appl
7	1280.8	31.2	1284	13	US-09-826-509-494	Sequence 494, App
8	521	12.7	560	13	US-10-101-510-59	Sequence 59, Appl
9	412.4	10.0	451	11	US-09-918-995-8960	Sequence 8960, Ap
10	395.8	9.6	4286	13	US-10-007-926A-177	Sequence 177, App
11	395.8	9.6	4286	13	US-09-921-406C-13	Sequence 13, Appl
12	395.8	9.6	4286	13	US-10-210-120-15	Sequence 15, Appl
13	395.8	9.6	4286	15	US-10-225-567A-113	Sequence 113, App
14	395.8	9.6	4301	9	US-09-931-157-2	Sequence 2, Appli
15	392.6	9.6	1329	13	US-09-826-509-496	Sequence 496, App
16	284.4	6.9	438	10	US-09-867-701-3320	Sequence 3320, Ap
c 17	155	3.8	170	13	US-10-007-926A-228	Sequence 228, App
c 18	147	3.6	592	9	US-09-962-436-531	Sequence 531, App
c 19	147	3.6	592	10	US-09-880-107-2060	Sequence 2060, Ap
c 20	147	3.6	592	10	US-09-954-531-917	Sequence 917, App
21	114.6	2.8	800	9	US-09-778-927A-27	Sequence 27, Appl
c 22	101	2.5	183337	15	US-10-020-141-5	Sequence 5, Appli
23	100	2.4	101	13	US-09-998-904-6	Sequence 6, Appli
24	91	2.2	1155	13	US-09-826-509-510	Sequence 510, App
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26	79.6	1.9	1413	15	US-10-225-567A-57	Sequence 57, Appl
27	78	1.9	1200	13	US-09-826-509-458	Sequence 458, App
28	68.6	1.7	1173	13	US-09-826-509-530	Sequence 530, App
29	68.6	1.7	1352	13	US-10-116-275-210	Sequence 210, App
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31	68.4	1.7	2595	9	US-09-160-116-11	Sequence 11, Appl
32	62.8	1.5	3673778	13	US-10-312-841-1	Sequence 1, Appli
33	62	1.5	1563	9	US-09-160-116-1	Sequence 1, Appli
c 34	61.6	1.5	316	13	US-10-029-386-26963	Sequence 26963, A
c 35	61.6	1.5	566	13	US-10-029-386-13263	Sequence 13263, A
36	60	1.5	60	13	US-09-908-975-14863	Sequence 14863, A
37	57	1.4	65	13	US-09-908-975-29571	Sequence 29571, A
38	57	1.4	5145	13	US-10-311-455-321	Sequence 321, App
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c 40	56.4	1.4	18624	13	US-10-311-455-1675	Sequence 1675, Ap
41	56.2	1.4	99116	13	US-10-298-122-1	Sequence 1, Appli
42	56	1.4	15548	13	US-10-311-455-2128	Sequence 2128, Ap
43	56	1.4	16766	13	US-10-311-455-2130	Sequence 2130, Ap
44	56	1.4	17491	13	US-10-240-485-127	Sequence 127, App
45	55.6	1.4	11015	13	US-10-204-708-55	Sequence 55, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-931-157-1

; Sequence 1, Application US/09931157

; Patent No. US20020082414A1

; GENERAL INFORMATION:

; APPLICANT: Imura, Hiroo

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; APPLICANT: Nakao, Kazuwa
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4105
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (485)...(1768)
; NAME/KEY: sig_peptide
; LOCATION: (485)...(544)
; NAME/KEY: mat_peptide
; LOCATION: (545)...(1768)
US-09-931-157-1

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Query Match          100.0%; Score 4105; DB 9; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTTCGTGCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
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Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
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Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
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Db    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
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Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

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Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
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Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTACGGGAATTGGGATTCC	1080
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Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
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Db	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
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Db	2581	TTCAATCAGATAGTTCTTTTTCACAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTAAATGTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTAAATGTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000

Db	2941	 GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840

Db	3781	CATCATATGTCAGTGCATATATGCCTATAAATATAAGCCATAGGTTTCACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTGAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTGAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAGTTTACAGAAACCTT	4105

US-10-007-926A-229

; Sequence 229, Application US/10007926A

; Publication No. US20030143539A1

; GENERAL INFORMATION:

APPLICANT: BERTUCCI, FRANCOIS

; APPLICANT: HOULGATTE, REMI

; APPLICANT: BIRNBAUM, DANIEL

APPLICANT: NGUYEN, CATHERINE

; APPLICANT: VIENS, PATRICE

APPLICANT: FERT, VINCENT

; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

FILE REFERENCE: 1546-R-00

; CURRENT APPLICATION NUMBER: US/10/007.926A

: CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: 60/254,090

PRIOR FILING DATE: 2000-12-08

; NUMBER OF SEO ID NOS: 468

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; SOFTWARE: PatentIn Ver. 2.1

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; SEO ID NO 229

; LENGTH: 4105

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: endothelin receptor type a (EDNRA) gene.

Query Match 100.0%; Score 4105; DB 13; Length 4105;

Best Local Similarity 100.0%; Pred. No. 0;

QY 1 GAATTTCGCGGCCGCCTCTTTCGGTCCCAGAGTGGAGTGGAAAGGTCTGGAGCTTTGGGAGG 60

[illegible]

Db	1	GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC	300
Db	241	GCAGTGCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCAGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCAGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCTGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCTGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTTATCGTGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTTATCGTGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900

Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTGCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTGCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740

Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Db	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640

Db	2581	 TTCAATCAGATAGTTCTTTTTTCAACAAGTTCAATACTGTTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	 AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	 TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	 ATGATTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	 CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	 TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	 GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAG	3060
Db	3001	 TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAG	3060
Qy	3061	GGCCCAAGTCACTTTTGTCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	 GGCCCAAGTCACTTTTGTCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	 AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	 GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	 TGTAGCAACCTTCTGCATTCTAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480



Db 3421 AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT 3480  
 Qy 3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA 3540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA 3540  
 Qy 3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT 3600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT 3600  
 Qy 3601 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA 3660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3601 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA 3660  
 Qy 3661 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG 3720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3661 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG 3720  
 Qy 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780  
 Qy 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840  
 Qy 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900  
 Qy 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960  
 Qy 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020  
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 Db 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020  
 Qy 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080  
 Qy 4081 TAAATATAAAGTTTACAGAAACCTT 4105  
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 Db 4081 TAAATATAAAGTTTACAGAAACCTT 4105

RESULT 3

US-10-101-510-370

; Sequence 370, Application US/10101510

; Publication No. US20030148295A1

; GENERAL INFORMATION:

; APPLICANT: WAN, JACKSON

; APPLICANT: WANG, YIXIN

; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE

; FILE REFERENCE: 15117.0012

; CURRENT APPLICATION NUMBER: US/10/101,510

; CURRENT FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: 60/276,947  
; PRIOR FILING DATE: 2001-03-20  
; NUMBER OF SEQ ID NOS: 805  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 370  
; LENGTH: 4105  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-101-510-370

Query Match 100.0%; Score 4105; DB 13; Length 4105;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60
      |||
Db      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCTGTCGAGCCCT 120
      |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCTGTCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
      |||
Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
      |||
Db    181 CATCCATCCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
      |||
Db    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
      |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
      |||
Db    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420

Qy    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480
      |||
Db    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
      |||
Db    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540

Qy    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600
      |||
Db    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600

Qy    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
      |||
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Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTGCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTGCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTCATGGTACCCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500

Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGGCAAC	1560
Db	1501		
Qy	1561	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGGCAAC	1560
Db	1561		
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561		
Qy	1621	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1621		
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621		
Qy	1681	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1681		
Qy	1681	CATGAACGGAAACAAGCATCCAGTGGAAGAACCACGATCAAAAACAACCAACACAGACCG	1740
Db	1681		
Qy	1741	CATGAACGGAAACAAGCATCCAGTGGAAGAACCACGATCAAAAACAACCAACACAGACCG	1740
Db	1741		
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741		
Qy	1801	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1801		
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801		
Qy	1861	AATCCTCTCGGAGAAAAAATCACAAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1861		
Qy	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861		
Qy	1921	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1921		
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921		
Qy	1981	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1981		
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAAATGAAGACTGTT	2040
Db	1981		
Qy	2041	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAAATGAAGACTGTT	2040
Db	2041		
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041		
Qy	2101	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2101		
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101		
Qy	2161	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2161		
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTTCAGCCAAACACA	2220
Db	2161		
Qy	2221	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTTCAGCCAAACACA	2220
Db	2221		
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221		
Qy	2281	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2281		
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281		
Qy	2340	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2340		

Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAAACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAAACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCCAAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCCAAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240

Db	3181	 ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTG	4080

Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080

Qy 4081 TAAATATAAAGTTTACAGAAACCTT 4105

||||||||||||||||||||||||||||||

Db 4081 TAAATATAAAGTTTACAGAAACCTT 4105

#### RESULT 4

US-10-225-567A-115

; Sequence 115, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 115

; LENGTH: 4105

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-115

Query Match 100.0%; Score 4105; DB 15; Length 4105;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

||||||||||||||||||||||||||||||||

Db 1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy 61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTCTGTCGAGCCCT 120

||||||||||||||||||||||||||||||||

Db 61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTCTGTCGAGCCCT 120

Qy 121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

||||||||||||||||||||||||||||||||

Db 121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy 181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

||||||||||||||||||||||||||||||||

Db 181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy 241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

||||||||||||||||||||||||||||||||

Db 241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy 301 CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCCTC 360

||||||||||||||||||||||||||||||||

Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	1080
Db	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200



Qy	1201	TATGCTCAATGCCACATCAAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAAATTTTTGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040

Qy	2041	AAATGAAACCGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCCCTTCAGCCAAACACA	2220
Db	2161	AGATTAAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCCCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCACAAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCACAAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAAACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAAACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTGTTAAATGTGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTGTTAAATGTGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTTGAAGTGGCCAGATGAGTTTATCATGTCACT	2940

Db	2881	 TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	 GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	 TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCCAAGTGAAGTCTTTTGGTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	 GGCCCAAGTGAAGTCTTTTGGTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	 AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	 GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCATAAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	 TGTAGCAACCTTCTGCATTCATAAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	 AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACCTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	 CACCTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Db	3601	 TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	 ATTTGTTGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAAATCTATTATTCCTGCGC	3780

Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTGAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTGAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAGTTTACAGAAACCTT	4105

US-09-919-497-12

; Sequence 12, Application US/09919497

; GENERAL INFORMATION:

; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

; CURRENT APPLICATION NUMBER: US/09/919,497

; PRIOR APPLICATION NUMBER: US 60/221,735

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; NUMBER OF SEQ ID NOS: 100
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; SEQ ID NO 12

; TYPE: DNA

US-09-919-497-12

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1624 CCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 1683

Qy            1684 GAACGGAACAAGCATCCAGTGGAGAACCACGATCAAAA CAACCA CAACACAGACCGGAG    1743  
               |||||

Db	75	GAACGGAACAAGCATCCAGTGGGAAGAACCCACGATCAAAAACAACCAACAACAGACCCGGAG	134
Qy	1744	CAGCCATAAGGACAGCATGAACTGACCACCCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1803
Db	135		194
Qy	1804	CAGCCATAAGGACAGCATGAACTGACCACCCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1863
Db	195		254
Qy	1864	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGAATCTCTTCTCTGATCCTT	1923
Db	255		314
Qy	1924	CTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	1983
Db	315		374
Qy	1984	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	2043
Db	375		434
Qy	2044	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAA	2103
Db	435		494
Qy	2104	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGGCTA	2163
Db	495		554
Qy	2164	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	2223
Db	555		614
Qy	2224	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2283
Db	615		674
Qy	2284	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2343
Db	675		734
Qy	2344	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2403
Db	735		794
Qy	2404	AGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAACA	2463
Db	795		854
Qy	2464	CAAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2523
Db	855		914
Qy	2524	GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTTAAATG	2583
Db	915		974
Qy	2584	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	2643
Db	975		1034

Qy	2584	AATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTCAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG	1153
Qy	2764	ATTCGGAATTTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTCGGAATTTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATT	2883
Db	1214	CTCCTATTCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATT	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGAGTAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGAGTAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCACCATTTCAGAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCACCATTTCAGAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813

Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCCATATTTTAGGACAGGTAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCCATATTTTAGGACAGGTAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTCACACCATTTTGTTTAGACA	3843
Db	2174	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTCACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	3903
Db	2234	ATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	2293
Qy	3904	CAGAAAGTCATAGATTTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	3963
Db	2294	CAGAAAGTCATAGATTTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	2353
Qy	3964	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	4023
Db	2354	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	2413
Qy	4024	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTA	4083
Db	2414	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTA	2473
Qy	4084	AATAAAAGTTTACAGAAACCTT	4105
Db	2474	AATAAAAGTTTACAGAAACCTT	2495

# RESULT 6

US-10-204-752-30

; Sequence 30, Application US/10204752

; Publication No. US20030152956A1

; GENERAL INFORMATION:

; APPLICANT: OHTANI, No. US20030152956A1iko

; APPLICANT: MATSUI, Keiko

; APPLICANT: YOSHIDA, Nei

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; APPLICANT:  SUGITA, Yuji
; APPLICANT:  IZUHARA, Kenji
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE
; FILE REFERENCE: SHZ-009US
; CURRENT APPLICATION NUMBER: US/10/204,752
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: JP 2000-396166
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-204-752-30

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Query Match          60.2%; Score 2470; DB 13; Length 2595;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      1624 CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 1683
          |||
Db      15   CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 74

Qy      1684 GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG 1743
          |||
Db      75   GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG 134

Qy      1744 CAGCCATAAGGACAGCATGAACTGACCACCCCTTAGAAGCACTCCTCGGTACTCCCATAAT 1803
          |||
Db      135  CAGCCATAAGGACAGCATGAACTGACCACCCCTTAGAAGCACTCCTCGGTACTCCCATAAT 194

Qy      1804 CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGAATCTCTTCTCTGATCCTT 1863
          |||
Db      195  CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGAATCTCTTCTCTGATCCTT 254

Qy      1864 CTTCTTAATTCACTCCACACCCCAAGAAGAAATGCTTTCCAAACCGCAAGGTAGACTG 1923
          |||
Db      255  CTTCTTAATTCACTCCACACCCCAAGAAGAAATGCTTTCCAAACCGCAAGGTAGACTG 314

Qy      1924 GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC 1983
          |||
Db      315  GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC 374

Qy      1984 TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA 2043
          |||
Db      375  TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA 434

Qy      2044 TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA 2103
          |||
Db      435  TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA 494

Qy      2104 GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAAACTTTAGAGA 2163
          |||
Db      495  GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAAACTTTAGAGA 554

Qy      2164 TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA 2223

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Db	555	 TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	 TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	 TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAACA	2403
Db	735	 AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	 CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	 GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	2583
Db	915	 GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	 AATCAGATAGTTCTTTTTTACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	 ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	 GTGCACTGTATATAGAAGTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	 ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTGTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTTC	2883
Db	1214	 CTCCTATTCTCTTAATTTTTGTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	2943
Db	1274	 CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	 AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	3063

Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTCTAAATCTTGTAAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTCTAAATCTTGTAAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCATATTTTAGGACAGGTAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	3843
Db	2174	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATT	3903
Db	2234	ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATT	2293

Qy 3904 CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 3963  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2294 CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 2353

Qy 3964 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 4023  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2354 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 2413

Qy 4024 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA 4083  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2414 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA 2473

Qy 4084 AATAAAAGTTTACAGAAACCTT 4105  
 ||||||||||||||||||||  
 Db 2474 AATAAAAGTTTACAGAAACCTT 2495

RESULT 7

US-09-826-509-494  
 ; Sequence 494, Application US/09826509  
 ; Publication No. US20030204073A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lehmann-Bruinsma, Karin  
 ; APPLICANT: Liaw, Chen W.  
 ; APPLICANT: Lin, I-Lin  
 ; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated  
 Known G  
 ; TITLE OF INVENTION: Protein-Coupled Receptors  
 ; FILE REFERENCE: AREN-207  
 ; CURRENT APPLICATION NUMBER: US/09/826,509  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/195,747  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: 09/170,496  
 ; PRIOR FILING DATE: 1998-10-13  
 ; NUMBER OF SEQ ID NOS: 589  
 ; SOFTWARE: PatentIn Version 2.1  
 ; SEQ ID NO 494  
 ; LENGTH: 1284  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-826-509-494

Query Match 31.2%; Score 1280.8; DB 13; Length 1284;  
 Best Local Similarity 99.8%; Pred. No. 1.6e-308;  
 Matches 1282; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 485 ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 544  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 60

Qy 545 GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCACTTTT 604  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCACTTTT 120

Qy 605 CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTACCC 664

Db	121	 CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	180
Qy	665	AGCAATGGCTCAATGCACAACTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAA	724
Db	181	 AGCAATGGCTCAATGCACAACTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAA	240
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	784
Db	241	 TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	300
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	301	 CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	360
Qy	845	AGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	361	 AGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	420
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	421	 CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	480
Qy	965	TTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	481	 TTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	540
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCTTTG	1084
Db	541	 GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCTTTG	600
Qy	1085	GTAAGTGGCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1144
Db	601	 GTAAGTGGCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	660
Qy	1145	GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	661	 GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	720
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	721	 CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	780
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	781	 GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	840
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	841	 GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	900
Qy	1385	CGTCGAGAAGTGGCAAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTC	1444
Db	901	 CGTCGAGAAGTGAACAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTC	960
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGA	1504

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Db          961 CCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGA 1020
Qy          1505 TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG 1564
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1021 TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG 1080
Qy          1565 AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC 1624
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1081 AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC 1140
Qy          1625 CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATG 1684
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1141 CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATG 1200
Qy          1685 AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC 1744
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1201 AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC 1260
Qy          1745 AGCCATAAGGACAGCATGAACTGA 1768
          ||||||||||||||||||
Db          1261 AGCCATAAGGACAGCATGAACTGA 1284

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# RESULT 8

US-10-101-510-59

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; Sequence 59, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-59

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Query Match          12.7%; Score 521; DB 13; Length 560;
Best Local Similarity 97.7%; Pred. No. 3.4e-119;
Matches 550; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

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Qy          2464 GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG 60
Qy          2524 GTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC 120
Qy          2584 AATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA 2643

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      |||
Db      121 AATCAGATAGTTCTTTTTCACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA 179
      |||
Qy      2644 ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA 2703
      |||
Db      180 ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA 239
      |||
Qy      2704 GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG 2763
      |||
Db      240 GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG 299
      |||
Qy      2764 ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC 2823
      |||
Db      300 ATTCAGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC 359
      |||
Qy      2824 CTCCTATTCTCTTAATTTTTTGTTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTC 2883
      |||
Db      360 CTCCTATTCTCTTAATTTTTTGTTAAATGTAACTGGCAGTAAAGCTTTTTTGATCATTC 419
      |||
Qy      2884 CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTTCAGTGAA 2943
      |||
Db      420 CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTTCAGTGAA 479
      |||
Qy      2944 AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA 3003
      |||
Db      480 AAATTAATACCCACAAATGGCACCAG--AACTTACGATTCTTCACTTCTTGGGGTTTTCA 537
      |||
Qy      3004 GTATGAACCTAACTCCCCACCCC 3026
      |||
Db      538 GTATGAACCTAACTCCCCACCCC 560

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RESULT 9

US-09-918-995-8960

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; Sequence 8960, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8960
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(451)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8960

```

Query Match 10.0%; Score 412.4; DB 11; Length 451;  
Best Local Similarity 98.6%; Pred. No. 3.6e-92;  
Matches 416; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	3347	AGTCCATTTTAAACCTGTAGCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATT	3406
Db	29	AATTCATTTTAAACCTGTAGCAACCTTTTGCATTTCATAAAATCTTGTAATCATGTTACCATT	88
Qy	3407	ACAAATGGGATATAAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGT	3466
Db	89	ACAAATGGTATATAAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGT	148
Qy	3467	TTTGTTTGGTTGGTTGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGG	3526
Db	149	TTTGTTTGGTTGGTTGGTTTGATAAAACAGTATTTGGGGTCATATTGATTTCCTGTGCTGG	208
Qy	3527	AGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGA	3586
Db	209	AGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGA	268
Qy	3587	TGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATA	3646
Db	269	TGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATA	328
Qy	3647	AATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCC	3706
Db	329	AATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCC	388
Qy	3707	AGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTA	3766
Db	389	AGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTA	448
Qy	3767	TT 3768	
Db	449	TT 450	

RESULT 10

US-10-007-926A-177

; Sequence 177, Application US/10007926A

; Publication No. US20030143539A1

; GENERAL INFORMATION:

; APPLICANT: BERTUCCI, FRANCOIS

; APPLICANT: HOULGATTE, REMI

APPLICANT: BIRNBAUM, DANIEL

; APPLICANT: NGUYEN, CATHERINE

; APPLICANT: VIENS, PATRICE

APPLICANT: FERT, VINCENT

10 TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

; FILE REFERENCE: 1546-R-00

; CURRENT APPLICATION NUMBER: US/10/007,926A

; CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: 60/254,090

; PRIOR FILING DATE: 2000-12-08

; NUMBER OF SEQ ID NOS: 468

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 177  
; LENGTH: 4286  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: endothelin receptor type b (EDNRB) gene.  
US-10-007-926A-177

Query Match 9.6%; Score 395.8; DB 13; Length 4286;  
Best Local Similarity 65.7%; Pred. No. 2.6e-87;  
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      689 TGCCACAGCAGACTAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564

Qy      749 ACTATTTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
      | | ||| | |||| | | |||| | | | | | | | | | | | | | |
Db      565 CTTGTGTTCTGTCTGGGGATCATCGGGAATCCACACTTCTGAGAATTATCTACAAGAAC 624

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868
      || | | ||| | | | | |||| | | | | | | | | | | | | |
Db      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
      | | | ||||| | | ||||| | | | | | | | | | | | | |
Db      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740

Qy      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTGCAGAAGTCCTCG 988
      ||||| | | | | | | | | | | | | | | | | | | | |
Db      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789

Qy      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048
      ||||| |||| | | | | | | | | | | | | | | | | | | |
Db      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849

Qy      1049 TCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC 1108
      || ||||| | | | | ||||| | | | | | | | | | | | |
Db      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909

Qy      1109 ATCTGGATCCTGTCTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTTCATGGTACCC 1168
      || ||| | | | | | | | | | | | | | | | | | | | |
Db      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969

Qy      1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
      | | | | | | | | | | | | | | | | | | | | | |
Db      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT 1029

Qy      1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282
      ||||| |||| | | | | | | | | | | | | | | | | | |
Db      1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTTG 1089

Qy      1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342
      || |||| | | |||| | | | | | | | | | | | | | | |
Db      1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1146

Qy      1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402
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      || | ||| || ||||| | | ||| || || ||||| || || ||||| || ||
Db      1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206

Qy      1403 ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT 1462
      || ||| || ||| |||| | | ||||| || ||||| || || ||||| || ||| |
Db      1207 ACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG 1266

Qy      1463 ATATTGAAGAAAAGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522
      || ||||| || ||| ||||| || | || || || ||||| || || |||
Db      1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTT 1326

Qy      1523 TTAAGTCTCATGGATTACATCGGTATTAACTTGGCAACCATGAATTCATGTATAAACCCC 1582
      | || | ||| || || ||||| || || ||||| || || ||||| || || |||||
Db      1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAAACCCA 1386

Qy      1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642
      || ||||| ||||| ||||| || || ||||| || || ||||| || ||||| |||||
Db      1387 ATTGCTCTGTATTTGGTGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGC 1446

Qy      1643 TGCTG 1647
      || ||
Db      1447 TGGTG 1451

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RESULT 11
US-09-921-406C-13
; Sequence 13, Application US/09921406C
; Publication No. US20030152923A1
; GENERAL INFORMATION:
; APPLICANT: Yakhini, Zohar
; APPLICANT: Ben-Dor, Amir
; APPLICANT: Sampas, Nick
; APPLICANT: Dougherty, Edward
; APPLICANT: Trent, Jeff
; APPLICANT: Meltzer, Paul
; APPLICANT: Chen, Yidong
; APPLICANT: Weeraratna, Ashani
; APPLICANT: Jiang, Yuan
; APPLICANT: Bittner, Michael
; TITLE OF INVENTION: Classifying Cancers
; FILE REFERENCE: 10010313-1
; CURRENT APPLICATION NUMBER: US/09/921,406C
; CURRENT FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-921-406C-13

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Query Match          9.6%;  Score 395.8;  DB 13;  Length 4286;
Best Local Similarity 65.7%;  Pred. No. 2.6e-87;
Matches 634;  Conservative 0;  Mismatches 307;  Indels 24;  Gaps 3;

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Qy      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACTGTGATATCTTGT 748
      |||| | | | | ||| | ||||| ||||| || || || || || || || || || ||

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Db	505	TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTGTGTCTCCTGC	564
Qy	749	ACTATTTTCATCGTGGAATGGTGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC	808
Db	565	CTTGTGTTCTGTGCTGGGGATCATCGGGAACCCACACTTCTGAGAATTATCTACAAGAAC	624
Qy	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC	868
Db	625	AAGTGCATGCGAAAACGGTCCC AATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	684
Qy	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Db	685	CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	740
Qy	929	GATCACAAATGACTTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTTG CAGAAGTCCTCG	988
Db	741	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC	789
Qy	989	GTGGGGATCACCGTCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC	1048
Db	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Qy	1049	TCCTGGAGTCGTGTT CAGGGAATTGGGATTCCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Db	850	TCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Qy	1109	ATCTGGATCCTGTCCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTCATGGTACCC	1168
Db	910	ATTTGGGTGGTCTCTGTGGTTC TGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAAACTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT	1029
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTC TATTTCTGTATG	1282
Db	1030	TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTT CAGTTTCTATTTCTGCTTG	1089
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	1090	CCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG	1146
Qy	1343	AATGGCAGCTTGAGAAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1147	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1206
Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTGGTTCCCTCTTCACTTAAGCCGT	1462
Db	1207	ACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGG	1266
Qy	1463	ATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1267	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT	1326
Qy	1523	TTACTGCTCATGGATTACATCGGTATTA ACTTGGCAACCATGAATTCATGTATAAAACCC	1582
Db	1327	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGCAATTAACCCA	1386

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Qy      1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1446

Qy      1643 TGCTG 1647
          || ||
Db      1447 TGGTG 1451

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# RESULT 12

US-10-210-120-15

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; Sequence 15, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-15

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Query Match          9.6%; Score 395.8; DB 13; Length 4286;
Best Local Similarity 65.7%; Pred. No. 2.6e-87;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
          ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564

Qy      749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
          | | ||| | |||| | | |||| | | | | | | | | | | | | | |
Db      565 CTTGTGTTCTGCTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 868
          || || ||| | | | | | | | | | | | | | | | | | | | |
Db      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
          | | ||||| | ||||| | | ||||| | | ||||| | | |||||
Db      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----- 740

Qy      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCAGAGAAGTCCTCG 988
          ||||| | | | | | | | | | | | | | | | | | | | |
Db      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789

```

Qy 989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048  
 ||||| ||||| || || | || || ||||| || ||||| || ||||| |||||  
 Db 790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849

Qy 1049 TCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC 1108  
 || ||||| || || | ||||| || ||||| || || || ||||| || ||  
 Db 850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909

Qy 1109 ATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTTCATGGTACCC 1168  
 || ||||| || || | ||||| || ||||| || ||||| || || || || || ||  
 Db 910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969

Qy 1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222  
 || || || | || | || | || || || || || || || || || || || || || || ||  
 Db 970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCTAGAAGACAGCT 1029

Qy 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282  
 ||||| ||||| |||| | || | || || || ||||| || || ||||| ||||| || ||  
 Db 1030 TTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTTG 1089

Qy 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342  
 || ||||| ||||| || || || || || || ||||| ||||| ||||| ||||| || || ||  
 Db 1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAG 1146

Qy 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402  
 || | || || || ||||| || || || || || ||||| || || ||||| ||||| || ||  
 Db 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206

Qy 1403 ACAGTTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT 1462  
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 Db 1207 ACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGG 1266

Qy 1463 ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522  
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 Db 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTGAGCTTT 1326

Qy 1523 TTAAGTCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC 1582  
 | || | |||| || || ||||| || || || || || ||||| || || ||||| || || || || ||  
 Db 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386

Qy 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642  
 || ||||| ||||| ||||| || || || || || || || || || || || || || || || || ||  
 Db 1387 ATTGCTCTGTATTTGGTGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1446

Qy 1643 TGCTG 1647  
 || ||  
 Db 1447 TGGTG 1451

RESULT 13  
 US-10-225-567A-113  
 ; Sequence 113, Application US/10225567A  
 ; Publication No. US20030113798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LifeSpan Biosciences  
 ; APPLICANT: Brown, Joseph P.

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; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-113

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Query Match          9.6%; Score 395.8; DB 15; Length 4286;
Best Local Similarity 65.7%; Pred. No. 2.6e-87;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
      |||| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564

Qy      749 ACTATTTTCATCGTGGGAATGGTGGGAATGCAACTCTGCTCAGGATCATTACCAGAAC 808
      |  |  ||| |  |||| |  |  |||| |  |  ||| |  |  ||| |  |  ||| |  |  ||| |
Db      565 CTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868
      ||  ||  ||| |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
      |  |  ||||| |  ||||| |  ||||| |  ||||| |  ||||| |  ||  ||||| |
Db      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740

Qy      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTCAGAAAGTCCTCG 988
      |||| |  |  |  ||||| |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789

Qy      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048
      |||| |  |||| |  ||  |  ||  |  |||| |  ||  ||||| |  ||  ||||| |
Db      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849

Qy      1049 TCCTGGAGTCGTGTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC 1108
      ||  ||||| |  ||  ||||| |  ||||| |  ||  ||  ||  ||  ||  ||  ||  ||
Db      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909

Qy      1109 ATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCC 1168
      ||  ||| |  |  ||  |  |||| |  ||||| |  ||||| |  ||  ||  ||  ||  ||
Db      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969

Qy      1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
      |  ||  ||  |  ||  |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT 1029

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Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG	1282
Db	1030	TTCATGCAGTTTACCAAGACAGCAAAAGATTGGTGGCTGTTCAATTTCTATTTCTGCTTG	1089
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG	1146
Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1147	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1206
Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT	1462
Db	1207	ACCGTCTTTTGCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACTCAGCAGG	1266
Qy	1463	ATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1267	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTGTAGCTTT	1326
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC	1582
Db	1327	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1386
Qy	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1642
Db	1387	ATTGCTCTGTATTTGGTGTGAGCAAAAGATTCAAAACTGCTTTAAGTCATGCTTATGCTGC	1446
Qy	1643	TGCTG	1647
Db	1447	TGGTG	1451

#### RESULT 14

US-09-931-157-2

```

; Sequence 2, Application US/09931157
; Patent No. US20020082414A1
; GENERAL INFORMATION:
; APPLICANT: Imura, Hiroo
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4301
; TYPE: DNA
; ORGANISM: Homo Sapiens

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; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (238)...(1566)  
US-09-931-157-2

Query Match 9.6%; Score 395.8; DB 9; Length 4301;  
Best Local Similarity 65.7%; Pred. No. 2.6e-87;  
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      689 TCCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564

Qy      749 ACTATTTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTACCAGAAC 808
      | | ||| | | | | | | | | | | | | | | | | | | | | | |
Db      565 CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740

Qy      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTTGCAGAAGTCCTCG 988
      ||||| | | | | | | | | | | | | | | | | | | | | |
Db      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC 789

Qy      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC 1048
      ||||| | | | | | | | | | | | | | | | | | | | | |
Db      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849

Qy      1049 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCCTTTGGTAACTGCCATTGAAATTGTCTCC 1108
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909

Qy      1109 ATCTGGATCCTGTCCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTCATGGTACCC 1168
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969

Qy      1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT 1029

Qy      1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282
      ||||| | | | | | | | | | | | | | | | | | | | | |
Db      1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG 1089

Qy      1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      1090 CCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1146

Qy      1343 AATGGCAGCTTGAGAAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206
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Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTGGCTGGTTCCCTCTTCACTTAAGCCGT	1462
Db	1207	ACCGTCTTTTGCCTGGTCCTTGCTCTTGGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGG	1266
Qy	1463	ATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1267	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTGTAGCTTT	1326
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAAC TTGGCAACCATGAATTCATGTATAAACCCC	1582
Db	1327	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1386
Qy	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1642
Db	1387	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC TGCTTAAAGTCATGCTTATGCTGC	1446
Qy	1643	TGCTG	1647
Db	1447	TGGTG	1451

Query Match 9.6%; Score 392.6; DB 13; Length 1329;  
Best Local Similarity 65.5%; Pred. No. 6.9e-87;  
Matches 632; Conservative 0; Mismatches 309; Indels 24; Gaps 3;



Db	328	CTTGTGTTTCGTGCTGGGGATCATCGGAACTCCACACTTCTGAGAATTATCTACAAGAAC	387
Qy	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC	868
Db	388	AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	447
Qy	869	TATGTGGTCAATTGATCTCCCTATCAAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Db	448	CACATCGTCATTGACATCCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	503
Qy	929	GATCACAAATGACTTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCGAGAAGTCCTCG	988
Db	504	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	552
Qy	989	GTGGGGATCACCGTCCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC	1048
Db	553	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	612
Qy	1049	TCCTGGAGTCGTGTTT CAGGGAATTGGGATTCTTTGGTAACTGCCATTGAAAATTGTCTCC	1108
Db	613	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAAATGGACAGCAGTAGAAAATTGTTTTG	672
Qy	1109	ATCTGGATCCTGTCTTTTATCCTGGCCATTCTCTGAAGCGATTGGCTTCGTTCATGGTACCC	1168
Db	673	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTGTATATAATTACG	732
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	733	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT	792
Qy	1223	TTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTATTTCTGTATG	1282
Db	793	TTTCATGCAGTTT TACAAGACAGCAAAAGATTGGTGGCTGTT CAGTTTCTATTTCTGCTTG	852
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAAG	1342
Db	853	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAAG	909
Qy	1343	AATGGCAGCTTGAGAAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	910	AAAAGTGGCATGCAGATTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGAAGAAA	969
Qy	1403	ACAGTTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT	1462
Db	970	ACCGTCTTTTTGCCTGGTCCCTTGTCTTTTGCCCTCTGCTGGCTTCCCTTCACTCAGCAGG	1029
Qy	1463	ATATTGAAGAAAAC TG GTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1030	ATTCTGAAGCTCACTCTTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTT	1089
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAAC TTGGCAACCATGAATTCATGTATAAACCC	1582
Db	1090	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAAACCA	1149
Qy	1583	ATAGCTCTGTATTTTTGTGAGCAAGAAATTTAAAAATGTTTCCAGTCATGCCTCTGCTGC	1642
Db	1150	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC TGCTTTAAGTCATGCTTATGCTGC	1209

Qy 1643 TGCTG 1647

|| ||

Db 1210 TGGTG 1214

Search completed: December 13, 2003, 00:41:34

Job time : 1215.3 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:16:56 ; Search time 949.825 Seconds  
(without alignments)  
11666.569 Million cell updates/sec

Title: US-09-931-157-1  
Perfect score: 4105  
Sequence: 1 gaattcgcgccgcctcttg.....taaaagtttacagaaacctt 4105

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:\*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*
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- 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	4105	100.0	4105	24	ABZ35259		Human gene express
2	4105	100.0	4105	24	ABV94238		Breast carcinoma r
3	4105	100.0	4105	25	ABZ42662		Human endothelin A
4	4103.4	100.0	4105	14	AAQ34583		ETa receptor gene.
5	4103	100.0	4105	21	AAA38341		Human endothelin r
6	4079	99.4	4079	25	ACA56659		Human signalling p
7	2470	60.2	2595	24	AAL39858		Human allergy-asso
8	2470	60.2	2595	24	ABK94408		DNA encoding endot
9	2470	60.2	2595	24	ABK35492		Human endometrial
10	1819.6	44.3	1868	21	AAF20903		Human low adenosin
11	1819.6	44.3	1868	21	AAF20915		Human endothelin r
12	1819.6	44.3	1868	21	AAA34781		Human adenosine re
13	1819.6	44.3	1868	21	AAA34793		Human adenosine re
14	1819.6	44.3	2008	21	AAF20904		Human low adenosin
15	1819.6	44.3	2008	21	AAA34782		Human adenosine re
16	1819.6	44.3	5036	21	AAF21447		Human endothelin r
17	1819.6	44.3	117609	21	AAF21435		Human receptor-rel
18	1296.8	31.6	1310	21	AAF20902		Human endothelin r
19	1296.8	31.6	1310	21	AAF20914		Human ELAM-1 polyn
20	1296.8	31.6	1310	21	AAA34780		Human adenosine re
21	1296.8	31.6	1310	21	AAA34792		Human adenosine re
22	1296.8	31.6	146981	21	AAF21442		Human ELAM-1 polyn
23	1280.8	31.2	1284	23	ABI97987		Non-endogenous hum
24	1248.8	30.4	1284	15	AAQ63209		Human endothelin r
25	521	12.7	560	24	ABZ34947		Human gene express
26	403.8	9.8	1965	13	AAQ25892		Sequence encodes e
27	399	9.7	4301	14	AAQ34584		ETb receptor gene.
28	396.6	9.7	1406	15	AAQ53922		Bovine ET receptor
29	395.8	9.6	1470	25	ACA56605		Human signalling p
30	395.8	9.6	1632	24	AAD24966		Human G-protein co
31	395.8	9.6	1719	21	AAF21285		Human low adenosin
32	395.8	9.6	1720	21	AAA35163		Human adenosine re
33	395.8	9.6	1872	21	AAF21283		Human low adenosin
34	395.8	9.6	1872	21	AAA35161		Human adenosine re
35	395.8	9.6	1873	19	AAV17875		Homo sapiens endot
36	395.8	9.6	4286	21	AAF21284		Human low adenosin
37	395.8	9.6	4286	21	AAA35162		Human adenosine re
38	395.8	9.6	4286	24	ABV94186		Breast carcinoma r
39	395.8	9.6	4286	25	ABZ42661		Human endothelin B
40	395.8	9.6	13611	21	AAF21288		Human low adenosin
41	395.8	9.6	13612	21	AAA35166		Human adenosine re
42	392.6	9.6	1329	23	ABI97988		Non-endogenous hum
43	383.2	9.3	1958	24	ABI99321		Mouse ischaemic co
44	381.2	9.3	1578	21	AAF21287		Human low adenosin
45	381.2	9.3	1578	21	AAA35165		Human adenosine re

# ALIGNMENTS

RESULT 1

ABZ35259

ID ABZ35259 standard; cDNA; 4105 BP.

XX

AC ABZ35259;

XX

DT 05-FEB-2003 (first entry)

XX

DE Human gene expression profile polynucleotide SEQ ID NO 370.

XX

KW Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;  
KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;  
KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;  
KW gene expression; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200274979-A2.

XX

PD 26-SEP-2002.

XX

PF 20-MAR-2002; 2002WO-US08456.

XX

PR 20-MAR-2001; 2001US-276947P.

XX

PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.

XX

PI Wan J, Wang Y;

XX

DR WPI; 2002-740862/80.

XX

PT New gene expression profile generated from primary, endothelial,  
PT epithelial, and muscle cell types, useful for identifying disease  
PT pathologies involving alterations of gene expression, e.g. cancer -

XX

PS Disclosure; Page 513-515; 850pp; English.

XX

CC The invention relates to a gene expression profile comprising one or more  
CC genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type  
CC is a coronary artery endothelium, umbilical artery or vein endothelium,  
CC aortic endothelium, dermal microvascular endothelium, pulmonary artery  
CC endothelium, myometrium microvascular endothelium, keratinocyte  
CC epithelium, bronchial epithelium, mammary epithelium, prostate  
CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,  
CC small airway epithelium, renal epithelium, umbilical artery smooth  
CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,  
CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,  
CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,  
CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,  
CC osteoblasts or prostate stromal cell. The gene expression profile is used  
CC for determining the level of RNA expression for a sample, determining the  
CC phenotype of a cell and distinguishing cell types. The gene or a protein  
CC expression profile is useful in identifying disease pathologies  
CC involving alterations of gene expression. The assessment of expression  
CC profiles may provide meaningful information with respect to tumour type  
CC and stage, treatment methods, and prognosis. The gene or protein

CC expression profile may also be used for creating microarrays. The  
CC microarray is useful for genetic and physical mapping of genomes, DNA  
CC sequencing, genetic or medical diagnosis, genotyping of organisms,  
CC confirming cell or tissue identifications and in identifying promising  
CC antibiotics, antiviral or antifungal agents.

XX

SQ Sequence 4105 BP; 1138 A; 859 C; 845 G; 1263 T; 0 other;

Query Match 100.0%; Score 4105; DB 24; Length 4105;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60
      |||
Db      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCT 120
      |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
      |||
Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
      |||
Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
      |||
Db    241 GCAGTGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
      |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
      |||
Db    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420

Qy    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480
      |||
Db    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
      |||
Db    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540

Qy    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600
      |||
Db    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600

Qy    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
      |||
Db    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660

Qy    661 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 720
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Db	661		ACCCAGCAATGGCTCAATGCACAAC	TATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721		CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780	
Db	721		CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780	
Qy	781		AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840	
Db	781		AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840	
Qy	841		AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900	
Db	841		AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900	
Qy	901		TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960	
Db	901		TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960	
Qy	961		GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020	
Db	961		GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020	
Qy	1021		TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080	
Db	1021		TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080	
Qy	1081		TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140	
Db	1081		TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140	
Qy	1141		TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200	
Db	1141		TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200	
Qy	1201		TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260	
Db	1201		TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260	
Qy	1261		CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320	
Db	1261		CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320	
Qy	1321		TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380	
Db	1321		TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380	
Qy	1381		GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440	
Db	1381		GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440	
Qy	1441		GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500	
Db	1441		GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500	
Qy	1501		CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560	

Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTTTAA	2400



QY	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
QY	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTTAA	2520
QY	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
QY	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
QY	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
QY	2701	TCAGTGCAGTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCAGTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
QY	2761	ATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
QY	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTAACTGGCAGTAAGTCTTTTTTGATCA	2880
QY	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
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QY	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
QY	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
QY	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
QY	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAACAATTGTAAATTTCTTTTAGCCC	3180
QY	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240

Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTTACACCATTTTGTTT	3840
Db	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTTACACCATTTTGTTT	3840
Qy	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTG	4080
Qy	4081	TAAAATAAAAAGTTTACAGAAACCTT	4105

Db 4081 TAAATATAAGTTTACAGAAACCTT 4105

RESULT 2

ABV94238

ID ABV94238 standard; cDNA; 4105 BP.

XX

AC ABV94238;

XX

DT 08-JAN-2003 (first entry)

XX

DE Breast carcinoma related nucleotide sequence SEQ ID NO:229.

XX

KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour;  
KW gene; ss.

XX

OS Homo sapiens.

XX

PN WO200246467-A2.

XX

PD 13-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-IB02811.

XX

PR 08-DEC-2000; 2000US-254090P.

PR 07-DEC-2001; 2001US-0007926.

XX

PA (IPSO-) IPSOGEN.

XX

PI Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;

XX

DR WPI; 2002-619023/66.

XX

PT Novel polynucleotide library useful in molecular characterization of a  
PT carcinoma, comprising a pool of polynucleotide sequences or its  
PT subsequences which are either underexpressed or overexpressed in tumor  
PT cells -

XX

PS Claim 1; Page 258-259; 401pp; English.

XX

CC The present invention describes a polynucleotide library (I) useful in  
CC the molecular characterisation of a carcinoma, comprising a pool of  
CC polynucleotides or its subsequences which are either underexpressed or  
CC overexpressed in tumour cells, and correspond to any of the  
CC polynucleotide sequences chosen from the 468 sequences given in ABV94010  
CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for  
CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting  
CC (M1) differentially expressed polynucleotide sequences which are  
CC correlated with a cancer, involves obtaining a polynucleotide sample from  
CC a patient, and reacting the polynucleotide sample obtained with a probe  
CC immobilised on a solid support, where the probe comprises any combination  
CC of the polynucleotide sequences of (I) or its expression products encoded  
CC by polynucleotide sequences of (I), and detecting the reaction product.  
CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)  
CC is useful in molecular characterisation of a carcinoma. (I) and (II) are  
CC useful for the prognosis or diagnostic of tumour, in differentiating a

CC normal cell from a cancer cell, detecting a hormone sensitive tumour  
CC cell, differentiating a tumour with lymph nodes from a tumour without  
CC lymph nodes, differentiating antracycline-sensitive tumours from  
CC antracycline-insensitive tumours, and classifying good and poor prognosis  
CC primary breast tumours. (I) is useful for large-scale molecular  
CC characterisation of breast cancer that help in prediction, prognosis and  
CC cancer treatment, and for detecting differentially expressed genes that  
CC correlated with a cancer.

XX

SQ Sequence 4105 BP; 1138 A; 859 C; 845 G; 1263 T; 0 other;

Query Match 100.0%; Score 4105; DB 24; Length 4105;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60
      |||
Db      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCGTGCGAGCCCT 120
      |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCGTGCGAGCCCT 120

Qy    121 CGCGCGCGGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
      |||
Db    121 CGCGCGCGGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
      |||
Db    181 CATCCATCCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
      |||
Db    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
      |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
      |||
Db    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420

Qy    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480
      |||
Db    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
      |||
Db    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540

Qy    541 CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC 600
      |||
Db    541 CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC 600

Qy    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTT 660
      |||
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Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACACTATTGCCACAGCAGACTAAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACACTATTGCCACAGCAGACTAAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTACGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTACGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500

Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340

Qy	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAAAATTTTCATTTCAGGTATTTTGTAAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAAATTTTCATTTCAGGTATTTTGTAAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGTCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGTCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGTATATGCATGTGTGTGAT	3240

Db	3181		ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241		GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241		GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301		GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301		GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361		TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361		TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421		AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421		AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481		TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481		TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541		CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541		CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601		TGTCTGATATTTCTTTTCACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601		TGTCTGATATTTCTTTTCACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661		ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661		ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721		CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721		CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781		CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781		CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841		ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841		ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901		ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901		ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961		TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961		TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021		AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTG	4080



Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080

Qy 4081 TAAAATAAAAAGTTTACAGAAACCTT 4105  
 |||||

Db 4081 TAAAATAAAAAGTTTACAGAAACCTT 4105

RESULT 3

ABZ42662

ID ABZ42662 standard; DNA; 4105 BP.

XX

AC ABZ42662;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human endothelin A receptor nucleotide SEQ ID NO:115.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US50107.

XX

PR 19-DEC-2000; 2000US-257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR P-PSDB; ABP81816.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating  
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
 PT cancer or autoimmune diseases -

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PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising:  
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular  
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;

CC and (2) an isolated antibody having high specificity and high affinity  
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and  
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting  
 CC an antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention.

XX

SQ Sequence 4105 BP; 1138 A; 859 C; 845 G; 1263 T; 0 other;

Query Match 100.0%; Score 4105; DB 25; Length 4105;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Db	1	GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCTGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCTGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCCTCCGCGCCACCCACCCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCCTCCGCGCCACCCACCCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTTCCTCAAATTTGCCT	480

Db	421	 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320

Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTGTATTAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTGTATTAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160

Qy	2161	AGATTAAACGACAAGATTTTCTACTTTTTTTTAAAGTGATTTTTTGTCCCTTCAGCCAAAACACA	2220
Db	2161	AGATTAAACGACAAGATTTTCTACTTTTTTTTAAAGTGATTTTTTGTCCCTTCAGCCAAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAAATTCCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAAATTCCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAAATCAATGTCAAGTACC AAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAAATCAATGTCAAGTACC AAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAAACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAAACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGT TAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGT TAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000

Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCAATTGTCAACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCAATTGTCAACCATTTCAAAG	3060
Qy	3061	GGCCCAAGTGAAGTTTGTCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCCAAGTGAAGTTTGTCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTGTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTGTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACCTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACCTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAAATCATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAAATCATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTACACCATTTTGTGTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTACACCATTTTGTGTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900

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      |||
Db      3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900
Qy      3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
      |||
Db      3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
Qy      3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
      |||
Db      3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
Qy      4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
      |||
Db      4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
Qy      4081 TAAAATAAAAGTTTACAGAAACCTT 4105
      |||
Db      4081 TAAAATAAAAGTTTACAGAAACCTT 4105

```

#### RESULT 4

AAQ34583

ID AAQ34583 standard; DNA; 4105 BP.

XX

AC AAQ34583;

XX

DT 25-MAR-2003 (updated)

DT 11-MAY-1993 (first entry)

XX

DE ETa receptor gene.

XX

KW Human; ETa; ETb; endothelin; receptor; transmembrane domain; N tail;

KW extracellular; cytoplasmic; C tail; post translational; bovine;

KW modification; ET-1 receptor; antagonist; circulatory system; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	CDS	485..1768
----	-----	-----------

FT		/*tag= a
----	--	----------

FT	sig_peptide	485..544
----	-------------	----------

FT		/*tag= b
----	--	----------

FT	mat_peptide	545..1765
----	-------------	-----------

FT		/*tag= c
----	--	----------

FT	polyA_signal	4084..4089
----	--------------	------------

FT		/*tag= d
----	--	----------

FT	misc_feature	1972..1976
----	--------------	------------

FT		/*tag= e
----	--	----------

FT		/function= Related with mRNA instability
----	--	--

FT	misc_feature	2059..2063
----	--------------	------------

FT		/*tag= f
----	--	----------

FT		/function= Related with mRNA instability
----	--	--

FT	misc_feature	2309..2313
----	--------------	------------

FT		/*tag= g
----	--	----------

FT		/function= Related with mRNA instability
----	--	--

FT	misc_feature	2386..2390
----	--------------	------------

FT		/*tag= h
----	--	----------

FT /function= Related with mRNA instability  
 FT misc\_feature 2680..2684  
 FT /\*tag= i  
 FT /function= Related with mRNA instability  
 FT misc\_feature 3252..3256  
 FT /\*tag= j  
 FT /function= Related with mRNA instability  
 FT misc\_feature 3944..3948  
 FT /\*tag= k  
 FT /function= Related with mRNA instability  
 XX  
 PN EP522868-A1.  
 XX  
 PD 13-JAN-1993.  
 XX  
 PF 10-JUL-1992; 92EP-0306347.  
 XX  
 PR 12-JUL-1991; 91JP-0172828.  
 XX  
 PA (SHIO ) SHIONOGI SEIYAKU KK.  
 XX  
 PI Imura H, Nakanishi S, Nakao K;  
 XX  
 DR WPI; 1993-010677/02.  
 DR P-PSDB; AAR30885.  
 XX  
 PT Human ETa and ETb endothelin receptors - for measuring endothelin  
 PT and screening for endothelin antagonists  
 XX  
 PS Claim 6; Fig 1; 39pp; English.  
 XX  
 CC The sequences given in AAQ34583-84 encode the human ETa and ETb  
 CC endothelin receptors respectively. ETa is a 427 amino acid protein  
 CC with a molecular weight of 48,726. ETb comprises 442 amino acids and  
 CC has a molecular weight of 49,629. ETa has a higher affinity for  
 CC endothelin (ET)-1 and ET-2, whereas ETb has no selectivity for ET-1,  
 CC ET-2 or ET-3. The receptors each contain seven transmembrane domains  
 CC and have an extracellular N tail and a cytoplasmic C tail. There are  
 CC several potential sites for post translational modification, these  
 CC sites are identical to those of bovine ET-1 receptor. ETa cDNA is  
 CC 91.2% homologous to bovine ET-1 receptor cDNA and ETb cDNA is 61.1%  
 CC homologous to that of bovine ETa-receptor. The receptor proteins are  
 CC useful as reagents for measuring the amount of ET or screening for  
 CC antagonists of the ET receptor when studying the circulatory system.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 4105 BP; 1138 A; 860 C; 844 G; 1263 T; 0 other;

Query Match 100.0%; Score 4103.4; DB 14; Length 4105;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCGCGCCCGCCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 GAATTCGCGCCCGCCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60  
 QY 61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTCGTGCGAGCCCT 120



Db	61	 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTCTTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACCATTTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCGAGGAAGTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC	300
Db	241	 GCAGTGCCCGAGGAAGTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTCTCCGGCTTCCTC	360
Db	301	 CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCGAGGCGCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	 TGGCCCGAGGCGCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	 CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	 CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	 AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960

Db	901	TAAGCTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTTGAGAAAGTCCTCGGTGGGGATCACCGTCTCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTTGAGAAAGTCCTCGGTGGGGATCACCGTCTCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAAACAAGCATCCAGTGGAAGAACACGATCAAAACAACCAACACAGACCG	1740
Db	1681	CATGAACGGAAACAAGCATCCAGTGGAAGAACACGATCAAAACAACCAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800

Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTCACTACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTCACTACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCCTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640

Qy	2641	AAAAATCAATGTCAAGTACCAAAAATGTTAATGTATGTGTGCATTTAACTCTGCCTGAGACTTT	2700
Db	2641	AAAAATCAATGTCAAGTACCAAAAATGTTAATGTATGTGTGCATTTAACTCTGCCTGAGACTTT	2700
Qy	2701	TCAGTGCACCTGTATATAGAAAGTCTAAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACCTGTATATAGAAAGTCTAAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTTCGGAAAATTTTCATTTCAGGTATTTGTAAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAAATTTTCATTTCAGGTATTTGTAAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTTCAAAG	3060
Qy	3061	GGCCCAAGTGAAGTCTTTTGGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCCAAGTGAAGTCTTTTGGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTAACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTAACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTTCATATTGTTTCTGTGCTGGAGCAAAAGTCATTA	3540

Db	3481	 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	 TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	 TAAAATAAAAGTTTACAGAAACCTT	4105

RESULT 5

AAA38341

ID AAA38341 standard; DNA; 4105 BP.

XX

AC AAA38341;

XX

DT 21-AUG-2000 (first entry)

XX

DE Human endothelin receptor type A gene coding region.

XX

KW Endothelin receptor type A gene; coding region;

KW polymorphism; polymorphic marker; cardiovascular disease;

KW myocardial infarction; unstable angina; hypertension; atherosclerosis;

KW stroke; prognosis; drug screening; treatment outcome; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200022166-A2.  
XX  
PD 20-APR-2000.  
XX  
PF 13-OCT-1999; 99WO-IB01678.  
XX  
PR 14-OCT-1998; 98US-0104286.  
PR 14-OCT-1998; 98US-0104302.  
XX  
PA (EURO-) EURONA MEDICAL AB.  
XX  
PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;  
XX  
DR WPI; 2000-318010/27.  
XX  
PT Assessing cardiovascular status in humans involves comparing test  
PT polymorphic pattern comprising polymorphic positions within genes  
PT encoding specific proteins, with reference polymorphic pattern -  
XX  
PS Disclosure; Page 125-126; 126pp; English.  
XX  
CC The invention relates to a novel method of assessing the cardiovascular  
CC status in an individual and to newly identified polymorphisms in the  
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II  
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,  
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic  
CC receptors 1 and 2. The method comprises determining the sequence at one  
CC or more polymorphic positions within these genes, and comparing the  
CC pattern of polymorphisms from the individual with a reference polymorphic  
CC pattern obtained from a population of individuals exhibiting a  
CC predetermined cardiovascular disease status. The polymorphic markers are  
CC useful for determining the predisposition of an individual to  
CC cardiovascular disorders such as myocardial infarction, unstable angina,  
CC hypertension, atherosclerosis and stroke. They are also useful for  
CC predicting the likely cardiovascular status of a patient given a  
CC treatment regimen comprising administration of cardiovascular drugs  
CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-  
CC blockers) or calcium channel blockers). One or more polymorphic markers  
CC provides a basis for predicting the outcome of a treatment regimen.  
CC Fragments of the genes comprising a polymorphic site may be used as  
CC primers and probes for detecting genetic polymorphisms or in molecular  
CC library arrays for high throughput screening. The genes, and the proteins  
CC they encode are useful in the screening of potential cardiovascular  
CC drugs. Determination of an individual's polymorphic pattern reduces or  
CC eliminates trial and error in selecting a treatment for a particular  
CC individual cardiovascular patient. It also provides the ability to  
CC eliminate patients from clinical trials who are predicted to be  
CC non-responsive, or at a risk for an adverse response, to a particular  
CC treatment regimen. Adverse results in an early trial can be evaluated to  
CC identify polymorphic patterns so that the adverse results can be  
CC correlated with a sub-population of the test population, permitting  
CC exclusion of such sub-populations from the treatment group. Beneficial  
CC drugs can be approved for use in the appropriate population, thereby

CC decreasing the number of patients required for a clinical trial, which in  
CC turn decreases the duration and cost of such trials. The present  
CC sequence represents the human endothelin receptor type A gene  
CC coding region (GenBank S57498). The polymorphic sites identified are  
CC 969C/T, 1005A/G, 1146A/G and 2485T/C.

XX

SQ Sequence 4105 BP; 1138 A; 859 C; 843 G; 1263 T; 2 other;

Query Match 100.0%; Score 4103; DB 21; Length 4105;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60
      |||
Db      1 GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTCGTGCGAGCCCT 120
      |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTCGTGCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
      |||
Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
      |||
Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC 300
      |||
Db    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
      |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
      |||
Db    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420

Qy    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480
      |||
Db    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
      |||
Db    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540

Qy    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600
      |||
Db    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600

Qy    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
      |||
Db    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660

Qy    661 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 720
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Db	661	 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTCAGAAAGTCCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTCAGAAAGTCCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAANNAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTCCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560



Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCAAAAACGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCAAAAACGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAAACGACAAGATTTTCTACTTTTFTTAAGTGATTTTTTGTCTTCAGCCAAAACACA	2220
Db	2161	AGATTAAACGACAAGATTTTCTACTTTTFTTAAGTGATTTTTTGTCTTCAGCCAAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAA	2400

Qy	2401	ACACAAATTTCTAAAGCTACAAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTTCTAAAGCTACAAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAACTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAACTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAAATGTTAACTGGCAGTAAGTCTTTTTTTCATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAAATGTTAACTGGCAGTAAGTCTTTTTTTCATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCAATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCAATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240

Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAAATTGTGCCCCGCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAAATTGTGCCCCGCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAAATACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAAATACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTCCACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTCCACCATTTTGTTTAG	3840
Qy	3841	ACAAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTG	4080
Db	4021	AGTAACTTTGTAGAAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTG	4080
Qy	4081	TAAAAATAAAAGTTTACAGAAACCTT	4105

|||||  
Db 4081 TAAATAAAAGTTTACAGAAACCTT 4105

RESULT 6

ACA56659

ID ACA56659 standard; cDNA; 4079 BP.

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AC ACA56659;

XX

DT 06-JUN-2003 (first entry)

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DE Human signalling pathway polynucleotide probe SEQ ID NO 1257.

XX

KW Human; probe; ss; array element; Parkinson's disease;

KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

XX

OS Homo sapiens.

XX

PN US6500938-B1.

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PD 31-DEC-2002.

XX

PF 30-JAN-1998; 98US-0016434.

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PR 30-JAN-1998; 98US-0016434.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Au-Young J, Seilhamer JJ;

XX

DR WPI; 2003-352189/33.

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PT Combination of polynucleotide probes, useful as array elements in a

PT microarray for monitoring the expression of a number of target

PT polynucleotides -

XX

PS Claim 1; SEQ ID NO 1257; 65pp; English.

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CC The invention relates to a combination which, comprises a number of  
CC polynucleotide probes comprising a sequence selected from one of the 1490  
CC sequences mentioned in the specification. The combination is useful as an  
CC array element in a microarray for monitoring the expression of a number  
CC of target polynucleotides. The microarray is particularly useful in the  
CC diagnosis and treatment of cancer and immunopathology and neuropathology.  
CC The microarray is useful in diagnostics and treatment regimens, drug  
CC discovery and development, toxicological and carcinogenicity studies,  
CC forensics and pharmacogenomics. The microarray is also useful for  
CC monitoring progression of diseases and for developing sophisticated  
CC profiles for the effects of currently available therapeutic drugs. The  
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
CC and genomic fragments and in research and diagnostic applications. The  
CC array can detect changes in expression in a large number of genes coding  
CC for different signaling pathway populations which can be used to diagnose  
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,  
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease



Db	661	 AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	720
Qy	725	TACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGCAACT	784
Db	721	 TACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGCAACT	780
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	781	 CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	840
Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	 AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901	 CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965	TTCCCCTTTTTGCAAGTCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961	 TTCCCCTTTTTGCAAGTCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTTG	1084
Db	1021	 GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTTG	1080
Qy	1085	GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1144
Db	1081	 GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1140
Qy	1145	GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	1141	 GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201	 CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	1261	 GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	1321	 GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTTGCTCTTTGCTGGTTC	1444
Db	1381	 CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTTGCTCTTTGCTGGTTC	1440
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	 CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTCTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1564

Db	1501	TGTGAATTACTTAGTCTTCTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1684
Db	1621	CAGTCATGCCTCTGCTGCTGCTGTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1744
Db	1681	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCATAATC	1804
Db	1741	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCATAATC	1800
Qy	1805	CTCTCGGAGAAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	CTCTCGGAGAAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1924
Db	1861	TTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
Qy	1925	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1984
Db	1921	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT'TAAAT	2044
Db	1981	GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT'TAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAGAGAT	2164
Db	2101	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCCCTTCAGCCAAACACAATAT	2224
Db	2161	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCCCTTCAGCCAAACACAATAT	2220
Qy	2225	GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2284
Db	2221	GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATA	2344
Db	2281	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATA	2340
Qy	2345	GTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAACAC	2404
Db	2341	GTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAACAC	2400

Qy	2405	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
Db	2401	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2524
Db	2461	GCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2520
Qy	2525	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTAAATTCAAAGTAATGCTTCA	2584
Db	2521	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTAAATTCAAAGTAATGCTTCA	2580
Qy	2585	ATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2644
Db	2581	ATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2640
Qy	2645	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCAG	2704
Db	2641	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCAG	2700
Qy	2705	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2764
Db	2701	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2760
Qy	2765	TTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2824
Db	2761	TTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2820
Qy	2825	TCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2884
Db	2821	TCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2880
Qy	2885	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2944
Db	2881	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2940
Qy	2945	AATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTTCAG	3004
Db	2941	AATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTTCAG	3000
Qy	3005	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAGGGCC	3064
Db	3001	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAGGGCC	3060
Qy	3065	CACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3124
Db	3061	CACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3120
Qy	3125	TCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATTT	3184
Db	3121	TCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATTT	3180
Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
Db	3181	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3240



Qy	3245	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3304
Db	3241	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3300
Qy	3305	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3364
Db	3301	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3360
Qy	3365	GCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3424
Db	3361	GCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480
Qy	3485	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3544
Db	3481	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3540
Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
Db	3541	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3600
Qy	3605	TGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3664
Db	3601	TGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3660
Qy	3665	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3844
Db	3781	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3840
Qy	3845	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTC	3904
Db	3841	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTC	3900
Qy	3905	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3964
Db	3901	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3960
Qy	3965	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4024
Db	3961	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4020
Qy	4025	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA	4083
Db	4021	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA	4079

RESULT 7

AAL39858

ID AAL39858 standard; DNA; 2595 BP.

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AC AAL39858;

XX

DT 05-SEP-2002 (first entry)

XX

DE Human allergy-associated gene SEQ ID No 30.

XX

KW Antiallergic; allergic disease; carboxypeptidase M; cathepsin C; CYP1B1;  
KW endoserine A receptor; osteoblast-specific factor 2; DD96; gene therapy;  
KW bronchial asthma; human; ds.

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OS Homo sapiens.

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PN WO200252006-A1.

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PD 04-JUL-2002.

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PF 21-DEC-2001; 2001WO-JP11287.

XX

PR 26-DEC-2000; 2000JP-0396166.

XX

PA (GENO-) GENOX RES INC.

XX

PI Ohtani N, Matsui K, Yoshida N, Sugita Y, Izuhara K;

XX

DR WPI; 2002-500763/53.

XX

PT Examining allergic diseases by changes in expression levels of six  
PT allergy-associated genes inducible by stimulation e.g. of airway  
PT epithelia cells with interleukin-4 or 13, also applicable in screening  
PT compounds -

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PS Disclosure; Page 79-80; 106pp; Japanese.

XX

CC The invention relates to a novel method for examining allergic diseases,  
CC comprising determining the expression level of a gene selected from  
CC carboxypeptidase M, cathepsin C, endoserine A receptor, osteoblast-  
CC specific factor 2, DD96 and CYP1B1 in the biological sample from a  
CC patient, and comparing the expression level with that in the sample of a  
CC healthy individual. The polynucleotides of the invention can be used to  
CC treat disorders by gene therapy. The method is useful for examining  
CC allergic diseases particularly bronchial asthma and its diagnosis, which  
CC is also applicable in screening candidate compounds for remedies. This  
CC polynucleotide sequence represents a human allergy-associated gene of the  
CC invention.

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SQ Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 other;

Query Match 60.2%; Score 2470; DB 24; Length 2595;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1624 CCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 1683  
|||||

Db	15	CCAGTCATGCCTCTGCTGCTGTTTACCAGTCCAAAAAGTCTGATGACCTCGGTCCCCAT	74
Qy	1684	GAACCGAACAAGCATCCAGTGGGAAGAACCCAGATCAAAACAACCAACACAGACCGGAG	1743
Db	75	GAACCGAACAAGCATCCAGTGGGAAGAACCCAGATCAAAACAACCAACACAGACCGGAG	134
Qy	1744	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1803
Db	135	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	194
Qy	1804	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	1863
Db	195	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	254
Qy	1864	CTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	1923
Db	255	CTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	314
Qy	1924	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	1983
Db	315	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	374
Qy	1984	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAAATGAAGACTGTTAAA	2043
Db	375	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAAATGAAGACTGTTAAA	434
Qy	2044	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGGCTA	2103
Db	435	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGGCTA	494
Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	2163
Db	495	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	TTAACGACAAGATTTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAAAACA	794
Qy	2404	CAAAATCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAAATCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914

Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	2583
Db	915	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTCAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTAACCTCTGCCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTAACCTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG	1153
Qy	2764	ATTTCGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTTCGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	1214	CTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGCCAGATGAGTTTATCATGTCAAGTAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGCCAGATGAGTTTATCATGTCAAGTAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753

RESULT 8  
ABK94408  
ID ABK94408 standard; DNA; 2595 BP.  
XX

AC ABK94408;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE DNA encoding endothelin receptor A (EDNRA), exon 8.  
 XX  
 KW Endothelin; EDN; endothelin converting enzyme; ECE; EDNRA;  
 KW endothelin receptor A; signaling system; cardiovascular disease;  
 KW coronary heart disease; hypertension; atherosclerosis; angiogenesis;  
 KW fatty acid metabolism; diabetes; familial hypercholesterolaemia;  
 KW forensic marker; transgenic animal; solid support; SNP;  
 KW cardiovascular regulator; gene; ds; single nucleotide polymorphism.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT variation replace(1830,G)  
 FT /\*tag= a  
 FT /standard\_name= "Single nucleotide polymorphism"  
 XX  
 PN WO200224747-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 31-AUG-2001; 2001WO-EP10087.  
 XX  
 PR 19-SEP-2000; 2000EP-0120123.  
 XX  
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
 XX  
 PI Brinkmann U, Hoffmeyer S;  
 XX  
 DR WPI; 2002-435060/46.  
 XX  
 PT Novel polynucleotide of the endothelin/endothelin converting  
 PT enzyme/receptors of endothelin and endothelin converting enzyme  
 PT signaling system associated with cardiovascular disease, useful for  
 PT treating the disease -  
 XX  
 PS Claim 1; Page -; 190pp; English.  
 XX  
 CC The invention describes a polynucleotide (I) of the endothelin  
 CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)  
 CC signaling system which is associated with a cardiovascular disease. (I),  
 CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)  
 CC or (II) is useful for producing cells capable of expressing a molecular  
 CC variant polypeptide which is associated with a cardiovascular disease.  
 CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing  
 CC a molecular variant gene comprising (I) is useful for identifying and  
 CC obtaining a pro-drug or drug capable of modulating the activity of a  
 CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system  
 CC or its gene product, or for identifying and obtaining an inhibitor of  
 CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE  
 CC signaling system or its gene product. The isolated proteins and  
 CC polynucleotides encoding them are useful for preparation of a  
 CC pharmaceutical composition for treating a cardiovascular disease such as  
 CC coronary heart disease, hypertension, atherosclerosis, or related to



Db	615	 TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	 TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAACA	2403
Db	735	 AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	 CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	 GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	2583
Db	915	 GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTACAAGTTCAATACGTTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	 AATCAGATAGTTCTTTTTTACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	 ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	 GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	 ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATT	2883
Db	1214	 CTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATT	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	2943
Db	1274	 CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	 AAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCACCATTTCAAAGGGC	3063
Db	1394	 GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123



Db	1454	CCACAGTGTACTTTTGGCTGGGCGATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTCTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTCTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	3543
Db	1874	TTTGATAAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAAAAAATACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCATATTTTAGGACAGGTAAAAAATACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	3843
Db	2174	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAAATGCATTTTATAAAAT	3903
Db	2234	ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAAATGCATTTTATAAAAT	2293
Qy	3904	CAGAAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	3963
Db	2294	CAGAAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	2353

Qy 3964 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 4023  
 |||  
 Db 2354 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 2413

Qy 4024 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA 4083  
 |||  
 Db 2414 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA 2473

Qy 4084 AATAAAAGTTTACAGAAACCTT 4105  
 |||  
 Db 2474 AATAAAAGTTTACAGAAACCTT 2495

# RESULT 9

ABK35492

ID ABK35492 standard; DNA; 2595 BP.

XX

AC ABK35492;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human endometrial cancer related gene, EDNRA.

XX

KW Human; ds; gene; endometrial cancer; differential expression;

KW DNA microarray; protein microarray.

XX

OS Homo sapiens.

XX

PN WO200209573-A2.

XX

PD 07-FEB-2002.

XX

PF 31-JUL-2001; 2001WO-US24104.

XX

PR 31-JUL-2000; 2000US-221735P.

XX

PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.

XX

PI Mutter GL;

XX

DR WPI; 2002-179967/23.

DR P-PSDB; AAU84272.

XX

PT Diagnosing endometrial cancer comprises determining expression of  
 PT nucleic acid molecules or expression products that are differentially  
 PT expressed in normal and malignant endometrium -

XX

PS Claim 1; Page 60-62; 233pp; English.

XX

CC The invention relates to diagnosing endometrial cancer in a subject  
 CC suspected of having endometrial cancer comprising determining the  
 CC expression of a set of nucleic acid molecules or expression products in  
 CC an endometrial sample suspected of being cancerous, where the set of  
 CC nucleic acid molecules comprises at least 2 nucleic acid molecules  
 CC selected from 50 fully defined sequences as given in the specification.  
 CC The nucleic acids are used as an array of at least 2 of the 50



Qy	2224	TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGGAAAAAAGACAAAAAT	2343
Db	675	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGGAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAAAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAAAAACA	794
Qy	2404	CAAATTTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAATTTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	2583
Db	915	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTTCGAAATTTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTTCGAAATTTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTTGTTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	1214	CTCCTATTCTCTTAATTTTTTGTTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCACTGAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCACTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123

Db	1454	 CCACAGTGACTTTTGGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	 ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	 TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	 ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	 TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	 AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	 GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	3543
Db	1874	 TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	 TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	 CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	 TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	3783
Db	2114	 GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	3843
Db	2174	 CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATT	3903
Db	2234	 ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATT	2293
Qy	3904	CAGAAAGTCATAGATTTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	3963

Db 2294 CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 2353  
 Qy 3964 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 4023  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2354 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 2413  
 Qy 4024 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA 4083  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2414 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA 2473  
 Qy 4084 AATAAAAGTTTACAGAAACCTT 4105  
 ||||||||||||||||||  
 Db 2474 AATAAAAGTTTACAGAAACCTT 2495

RESULT 10

AAF20903

ID AAF20903 standard; DNA; 1868 BP.

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AC AAF20903;

XX

DT 14-MAR-2001 (first entry)

XX

DE Human low adenosine antisense oligonucleotide #2470.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.

XX

PD 26-OCT-2000.

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PF 24-MAR-2000; 2000WO-US08020.

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PR 06-APR-1999; 99US-0127958.

XX

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX

PI Nyce JW;

XX

DR WPI; 2000-679539/66.

XX

PT Low adenosine (A) content antisense oligonucleotides which do not  
 PT trigger adenosine receptors during metabolism, useful e.g. for treating  
 PT cancers and respiratory obstructions -

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PS Disclosure; Page 676; 1592pp; English.

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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

XX

SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 other;

Query Match 44.3%; Score 1819.6; DB 21; Length 1868;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY            421 AAAAAAGTGAAGGTGTA AAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT    480  
               |||||

Db 10 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 69

QY            481 CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT    540  
               |||||

Db 70 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAAT 129

Qy            541 CAGTGATAATCCTGAGAGATA CAGCACAAATCTAAGCAATCATGTGGATGATTTCCACCAC     600  
             | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 130 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACACCAC 189

Qy           601 TTTTCGTGGCACAGAGCTCAGCTTCTGTTACCACTCATCAACCCACTAATTTGGTCCT     660  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 190 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 249

Qy           661 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 720  
             | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 250 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAAATTACTTCAGCTTT 309

Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGCGGAATGGTGGGGAATGC	780
Db	310	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGCGGAATGGTGGGGAATGC	369
Qy	781	AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	370	AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	429
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	430	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	489
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	490	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	549
Qy	961	GCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	550	GCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	609
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	610	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	669
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTCTTTATCCTGGCCATTCC	1140
Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGCTCTTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGCTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1090	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1149





DE Human endothelin receptor A polynucleotide fragment #2482.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200062736-A2.  
XX  
PD 26-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US08020.  
XX  
PR 06-APR-1999; 99US-0127958.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-679539/66.  
XX  
PT Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -  
XX  
PS Disclosure; Page 244; 1592pp; English.  
XX  
CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
CC and/or surfactant hypoproduction which are associated with a disease or

CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention.

XX

SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 other;

Query Match 44.3%; Score 1819.6; DB 21; Length 1868;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

```
Qy      421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGAATAAGAGATATTTTCCTCAAATTTGCCT 480
      |||
Db      10 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGAATAAGAGATATTTTCCTCAAATTTGCCT 69

Qy      481 CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
      |||
Db      70 CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 129

Qy      541 CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC 600
      |||
Db      130 CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC 189

Qy      601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
      |||
Db      190 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 249

Qy      661 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 720
      |||
Db      250 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 309

Qy      721 CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGAATGC 780
      |||
Db      310 CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGAATGC 369

Qy      781 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT 840
      |||
Db      370 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT 429

Qy      841 AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT 900
      |||
Db      430 AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT 489

Qy      901 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA 960
      |||
Db      490 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA 549

Qy      961 GCTGTTCCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT 1020
      |||
Db      550 GCTGTTCCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT 609

Qy      1021 TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGGAATTGGGATTCC 1080
      |||
```

Db	610	TAGTGTGGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCC	669
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTTTCTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1090	CCGATGTGAATTACTTAGTTTTCTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1150	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1209
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1210	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1269
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1270	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1329
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1330	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1390	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1449
Qy	1861	CTTCTTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1450	CTTCTTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1509

Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1510	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1569
Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1570	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	1629
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATG	2099
Db	1630	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAAACTTTA	2159
Db	1690	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAAACTTTA	1749
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	2218
Db	1750	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	1809
Qy	2219	CAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	2268
Db	1810	CAATATGGGCTCAAGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	1859

RESULT 12

AAA34781

ID AAA34781 standard; DNA; 1868 BP.

XX

AC AAA34781;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide SEQ ID NO:2470.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

XX

PR 03-AUG-1998; 98US-0095212.

XX

PA (UYEC-) UNIV EAST CAROLINA.

XX

[illegible]

Db	190	TTTTCGTGGCACAAGAGCTCAGCTTCTCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	249
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	250	ACCCAGCAATGGCTCAATGCACAACTATTTGCCACAGCAGACTAAAATTACTTCAGCTTT	309
Qy	721	CAAATACATTAACTGTGATATCTTGCTACTATTTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	310	CAAATACATTAACTGTGATATCTTGCTACTATTTTTCATCGTGGGAATGGTGGGGAATGC	369
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	370	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	429
Qy	841	AGCCAGTCTTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	430	AGCCAGTCTTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	489
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGTATCACAATGACTTTTGGCGTATTTCTTTGCAA	960
Db	490	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGTATCACAATGACTTTTGGCGTATTTCTTTGCAA	549
Qy	961	GCTGTTCCCTTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	550	GCTGTTCCCTTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	609
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	610	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	669
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTCTTTATCCTGGCCATTCC	1140
Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACCTGCGATCTTCTACACCCTCATGAC	1320
Db	850	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACCTGCGATCTTCTACACCCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAAATGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAAATGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAAAGTCTTCTGCTTGGTTGTAAATTTTGTCTCTTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAAAGTCTTCTGCTTGGTTGTAAATTTTGTCTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAGATGGACAAGAA	1089

Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1090	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1150	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1209
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1210	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1269
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1270	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1329
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1330	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGAATCTCTTCTCTGATC	1860
Db	1390	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGAATCTCTTCTCTGATC	1449
Qy	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1450	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1509
Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1510	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1569
Qy	1980	ATTCTGCGTGTTGTATTACAGCACTAAAAAATGGTGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1570	ATTCTGCGTGTTGTATTACAGCACTAAAAAATGGTGAGCTGGGGGAGAATGAAGACTGT	1629
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	2099
Db	1630	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTA	2159
Db	1690	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTA	1749
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	2218
Db	1750	GAGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	1809
Qy	2219	CAATATGGGCTCAGGTCACTTTTATTGAAATGTCATTTGGTGCCAGTAT	2268
Db	1810	CAATATGGGCTCAGGTCACTTTTATTGAAATGTCATTTGGTGCCAGTAT	1859

## RESULT 13

ID AAA34793 standard; DNA: 1868 BP.



XX  
 AC AAA34793;  
 XX  
 DT 28-JUL-2000 (first entry)  
 XX  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2482.  
 XX  
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200009525-A2.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 03-AUG-1999; 99WO-US17712.  
 XX  
 PR 03-AUG-1998; 98US-0095212.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW;  
 XX  
 DR WPI; 2000-205971/18.  
 XX  
 PT New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers -  
 XX  
 PS Disclosure; Page 645-646; 1343pp; English.  
 XX  
 CC The present invention describes a new composition comprising an  
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
 CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasise to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of  
 CC the ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present



Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTTTCTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1090	CCGATGTGAATTACTTAGTTTTCTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1150	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1209
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1210	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1269
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1270	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1329
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1330	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1390	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1449
Qy	1861	CTTCTTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1450	CTTCTTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1509

Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCCTTAATTGATCTAATTTACAT 	1979
Db	1510	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCCTTAATTGATCTAATTTACAT	1569
Qy	1980	ATTCTGCGTGTTGTATTCAAGCATAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT 	2039
Db	1570	ATTCTGCGTGTTGTATTCAAGCATAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	1629
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTTGCATGAAAATAGAGCTTTCAGTACATG 	2099
Db	1630	TAAATGAAACCAGAAGGATATTTACTACTTTTTGCATGAAAATAGAGCTTTCAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCAACCATGAAACTTTA 	2159
Db	1690	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCAACCATGAAACTTTA	1749
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA 	2218
Db	1750	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	1809
Qy	2219	CAATATGGGCTCAGGTCACCTTTATTTGAAATGTCATTGGTGCCAGTAT	2268
Db	1810	CAATATGGGCTCAGGTCACCTTTATTTGAAATGTCATTGGTGCCAGTAT	1859

AAAF20904

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SO

Query Match 44.3%; Score 1819.6; DB 21; Length 2008;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCT	480
Db	150	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCCCTCAAATTTGCCT	209
Qy	481	CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	210	CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	269
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600

Db	270	 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCAC	329
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	330	 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	389
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	390	 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	449
Qy	721	CAAATACATTAACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	450	 CAAATACATTAACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	509
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	510	 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	569
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	570	 AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	629
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	630	 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	689
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	690	 GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	749
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	750	 TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	809
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	810	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	869
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	870	 TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	929
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	930	 TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	989
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	990	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1049
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1050	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1109
Qy	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440

Db	1110	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1169
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1170	GTTCCCTCTTCATTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1229
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1230	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1289
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1290	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1349
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1350	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1409
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1410	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1469
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1470	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1529
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1530	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1589
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1590	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1649
Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1650	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1709
Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1710	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGAGCTGGGGGAGAATGAAGACTGT	1769
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	2099
Db	1770	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	1829
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTA	2159
Db	1830	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTA	1889
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	2218
Db	1890	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTTGTCTTCAGCCAAACA	1949
Qy	2219	CAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	2268
Db	1950	CAATATGGGCTCAAGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	1999

RESULT 15

AAA34782

ID AAA34782 standard; DNA; 2008 BP.

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AC AAA34782;

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DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide SEQ ID NO:2471.

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KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

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OS Homo sapiens.

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PN WO200009525-A2.

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PD 24-FEB-2000.

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PF 03-AUG-1999; 99WO-US17712.

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PR 03-AUG-1998; 98US-0095212.

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PA (UYEC-) UNIV EAST CAROLINA.

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PI Nyce JW;

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DR WPI; 2000-205971/18.

XX

PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers -

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PS Disclosure; Page 607; 1343pp; English.

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CC The present invention describes a new composition comprising an  
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including



CC breast and prostate cancer. The reduction of the adenosine content of  
CC the ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
CC differ from the previously named sequences. SEQ ID NO:11 to 1680  
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present  
CC invention. N.B. Sequences given in the disclosure of the present  
CC invention do not match up with their corresponding SEQ ID NO: sequences  
CC given in the sequence listing.

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SQ Sequence 2008 BP; 563 A; 463 C; 416 G; 566 T; 0 other;

Query Match 44.3%; Score 1819.6; DB 21; Length 2008;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTTCCTCAAATTTGCCT	480
Db	150	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTTCCTCAAATTTGCCT	209
Qy	481	CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	210	CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	269
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Db	270	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCAC	329
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	330	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	389
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	390	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	449
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	450	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	509
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	510	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	569
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	570	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	629
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	630	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	689
Qy	961	GCTGTTCCCTTTTTCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020

Db	690	GCTGTTCCCTTTTTCAGAAAGTCCTCGGTGGGATCACCGTCTCAACCTCTGCGCTCT	749
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTACAGGGAATTGGGATTCC	1080
Db	750	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTACAGGGAATTGGGATTCC	809
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	810	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	869
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	870	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	929
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	930	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	989
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCCTCATGAC	1320
Db	990	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCCTCATGAC	1049
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1050	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1109
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1440
Db	1110	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1169
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1170	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1229
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1230	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1289
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1290	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1349
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1350	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1409
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCAAGATCAAAAACAACCAACACAGACCG	1740
Db	1410	CATGAACGGAACAAGCATCCAGTGGAAGAACCAAGATCAAAAACAACCAACACAGACCG	1469
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1470	GAGCAGCCATAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1529
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1530	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1589

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Job time : 960.825 secs

Search completed: December 12, 2003, 11:27:08  
Job time : 960.825 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:16:57 ; Search time 14402.7 Seconds  
(without alignments)  
11659.930 Million cell updates/sec

Title: US-09-931-157-1  
Perfect score: 4105  
Sequence: 1 gaattcgcgccgcctcttg.....taaaagtttacagaaacctt 4105

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :: GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
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 32: em\_htg\_other:\*  
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 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%		Query		DB		ID	Description
No.	Score	Match	Length	DB	ID			
1	4105	100.0	4105	6	AR177879			AR177879 Sequence
2	4105	100.0	4105	6	AX548830			AX548830 Sequence
3	4105	100.0	4105	6	AX587759			AX587759 Sequence
4	4105	100.0	4105	6	E07649			E07649 cDNA encodi
5	4105	100.0	4105	9	HSET1R			X61950 H.sapiens m
6	4103	100.0	4105	9	S57498			S57498 endothelin
7	4101	99.9	4101	9	HUMETN1R			D90348 Homo sapien
8	4079	99.4	4079	6	AR270694			AR270694 Sequence
9	3183.2	77.5	3305	9	S45956			S45956 endothelin
10	2609.6	63.6	2705	9	BC022511			BC022511 Homo sapi
11	2470	60.2	2595	6	BD169895			BD169895 Method fo
12	2470	60.2	2595	9	D11144S8			D11151 Homo sapien
13	2409.2	58.7	164920	9	AC093908			AC093908 Homo sapi
14	2292	55.8	2337	11	G06463			G06463 human STS W
15	1819.6	44.3	1868	9	S63938			S63938 A-type endo
16	1786.6	43.5	3216	4	BTBETREC			X57765 Bovine mRNA
17	1560.2	38.0	1661	9	S67127			S67127 endothelin
18	1359	33.1	1359	9	S81539			S81539 endothelin-
19	1296.8	31.6	1310	9	HUMEDNRA			L06622 Homo sapien
20	1280.8	31.2	1284	6	AX280871			AX280871 Sequence
21	1280.8	31.2	1284	9	AY275462			AY275462 Homo sapi
22	1122	27.3	1374	4	S80652			S80652 endothelin
23	1103.2	26.9	1284	4	AF416703			AF416703 Ovis arie
24	1088.2	26.5	2696	10	BC008277			BC008277 Mus muscu
25	1048.8	25.5	1180	4	AF311974			AF311974 Oryctolag
26	1021	24.9	1021	11	G10643			G10643 human STS C
27	997	24.3	1436	10	RATENDOR			M60786 Rat endothe
28	951	23.2	1160	9	S81542			S81542 endothelin-
29	765.8	18.7	2944	5	AF040634			AF040634 Gallus ga
30	765.8	18.7	2988	5	AF472618			AF472618 Gallus ga
31	695	16.9	1032	9	S81545			S81545 endothelin-
32	635	15.5	3767	5	BC044316			BC044316 Xenopus l
33	632.8	15.4	1650	5	XLU06633			U06633 Xenopus lae

C	34	624.6	15.2	810	10	AF039892	AF039892 Mus muscu
	35	514	12.5	530	9	MFU20577	U20577 Macaca fasc
	36	492.4	12.0	531	9	D11144S2	D11145 Homo sapien
	37	487.4	11.9	1435	9	S55547S2	S55772 ETA=endothe
	38	487.4	11.9	66264	2	AC110065	AC110065 Homo sapi
	39	435.6	10.6	3157	5	BC048223	BC048223 Xenopus l
	40	425	10.4	1308	5	CCEDNRB2	Y16089 Coturnix co
	41	423.4	10.3	2225	5	AF472617	AF472617 Gallus ga
	42	411.6	10.0	1724	5	AB045356	AB045356 Oryzias l
	43	411	10.0	1314	4	AF276427	AF276427 Canis fam
44	407.8	9.9	1311	4	AF038900	AF038900 Equus cab	
45	407.8	9.9	1452	4	AF034530	AF034530 Canis fam	

## ALIGNMENTS

## RESULT 1

AR177879

LOCUS AR177879 4105 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 1 from patent US 6313276.

ACCESSION      AR177879

VERSION AR177879.1 GI:17920234

## KEYWORDS

SOURCE                      Unknown.

ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Imura, H., Nakao, K. and Nakanishi, S.

TITLE Human endothelin receptor

JOURNAL Patent: US 6313276-A 1 06-NOV-2001;

FEATURES	Location/Qualifiers
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source      1.  .4105
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/organism="unknown"

BASE COUNT	1138 a	859 c	845 g	1263 t
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ORIGIN

Query Match 100.0%; Score 4105; DB 6; Length 4105;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTTCGCGGCCGCCTCTTTCGCGTCCCAGAGTGGAGTGGAAAGGTCTGGAGCTTTGGGAGG 60

Db 1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

Qy 61 AGACGGGGAGGACAGACTGGAGGCGTGTTTCCTCCGGAGTTTTCTTTTCGTGCGAGCCCT 120  
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Db 61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTTCCGGAGTTTTCTTTTCGTGCGAGCCCT 120

Qy 121 CGCGCGCGGTACAGTCATCCGCTGGTCTGACGATTGTGGAGAGGCCGGTGGAGAGGCCTT 180  
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Db 121 CGCGCGCGGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy 181 CATCCATCCCACCGGTGTCGTCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240  
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Db 181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy	241	GCAGTGGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAATATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAATATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGGAATTGGGATTCC	1080
Db	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140

Db	1081	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	 TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	 TATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTGGCAAC	1560
Db	1501	 CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAAACACCACAACACAGACCG	1740
Db	1681	 CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAAACACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	 GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	 AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980



Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820

Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660

Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAGTTTACAGAAACCTT	4105

# RESULT 2

AX548830

LOCUS AX548830 4105 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 115 from Patent WO02061087.

ACCESSION AX548830

VERSION AX548830.1 GI:25813724

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.

TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides

JOURNAL Patent: WO 02061087-A 115 08-AUG-2002;

Lifespan Biosciences, Inc. (US)

FEATURES

source Location/Qualifiers

1. .4105

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

BASE COUNT 1138 a 859 c 845 g 1263 t

## ORIGIN

Query Match 100.0%; Score 4105; DB 6; Length 4105;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCGTGCGAGCCCT 120
        |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCGTGCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
        |||
Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
        |||
Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCGAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
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Db    241 GCAGTGCCCGAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
        |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCGAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
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Qy    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480
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Db    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
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Qy    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
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Db    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660

Qy    661 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 720
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Db    661 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 720

Qy    721 CAAATACATTAACACTGTGATATCTTGTAATTTTTCATCGTGGGAATGGTGGGGAATGC 780
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Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
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Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
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Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
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Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620

Qy	1621	TTTCCAGTCAATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCAATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGGAAGAACACGATCAAAAACAACCAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGGAAGAACACGATCAAAAACAACCAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACGAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACGAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTTATTTTTTAA	2520

Db	2461	 TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	 ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	 TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	 AAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	 TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	 ATGATTTCGGAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	 CACCTCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	 TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	 GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAG	3060
Db	3001	 TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	 GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	 AAAATCTTTTACTAGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360

Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCAACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCAACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAAGTTTACAGAAACCTT	4105



LOCUS AX587759 4105 bp DNA linear PAT 10-JAN-2003  
 DEFINITION Sequence 229 from Patent WO0246467.  
 ACCESSION AX587759  
 VERSION AX587759.1 GI:28212399  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.  
 REFERENCE 1  
 AUTHORS Bertucci,F., Houlgatte,R., Birnbaum,D., Nguyen,C., Viens,P. and  
 Fert,V.  
 TITLE Gene expression profiling of primary breast carcinomas using arrays  
 of candidate genes  
 JOURNAL Patent: WO 0246467-A 229 13-JUN-2002;  
 Ipsogen (FR)  
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 BASE COUNT 1138 a 859 c 845 g 1263 t  
 ORIGIN

Query Match 100.0%; Score 4105; DB 6; Length 4105;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420

Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTTCCTCAAATTTGCCT	480
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Qy	481	CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
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Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
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Qy	721	CAAATACATTAACTGTGATATCTTGTAATAATTTTCATCGTGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACTGTGATATCTTGTAATAATTTTCATCGTGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTCGAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTCGAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320

Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	 CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	 CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	 GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	 AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	 CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTGAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	 TTCTGCGTGTTGTATTGAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	 AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160

Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Db	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
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Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
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Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000

Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCAATTGTCACCATTTCAAAG	3060
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Qy	3061	GGCCACACAGTGACTTTTGGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
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Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
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Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
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Qy	3301	GTCTGAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAAACC	3360
Db	3301	GTCTGAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACCTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACCTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTCACACCATTTTGTGTTAG	3840
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 Db 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900

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 Db 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960

Qy 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020  
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 Db 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020

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Qy 4081 TAAAATAAAAGTTTACAGAAACCTT 4105  
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 Db 4081 TAAAATAAAAGTTTACAGAAACCTT 4105

RESULT 4

E07649

LOCUS E07649 4105 bp RNA linear PAT 29-SEP-1997

DEFINITION cDNA encoding endothelin receptor, ETA-receptor.

ACCESSION E07649

VERSION E07649.1 GI:2175784

KEYWORDS JP 1994157595-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Imura, H., Nakao, I. and Nakanishi, S.

TITLE HUMAN ENDOTHELIN RECEPTOR

JOURNAL Patent: JP 1994157595-A 1 03-JUN-1994;  
 SHIONOGI & CO LTD

COMMENT OS Homo sapiens (human)

PN JP 1994157595-A/1

PD 03-JUN-1994

PF 12-JUL-1991 JP 1991172828

PI IMURA HIROO, NAKAO ICHIKAZU, NAKANISHI SHIGETADA PC

C07K13/00, C12N5/10, C12N15/12, C12P21/02, (C12N5/10, C12R1:91), PC  
 (C12P21/02,

PC C12R1:91);

CC strandedness: Double;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

FH Key Location/Qualifiers

FH

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FT /tissue\_type='placenta'

FT /clone='phETIR'

FT 5'UTR 1. .484

FT CDS 485. .1768

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ORIGIN

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Query Match          . 100.0%;  Score 4105;  DB 6;  Length 4105;
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Qy    301 CGGAGCCCGGGACACCGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
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Qy    361 TGGCCCAGGCGCCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
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Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
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Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440



Db	1381		GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTGCTG	1440
Qy	1441		GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441		GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501		CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501		CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561		CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561		CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621		TTTCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621		TTTCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681		CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681		CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741		GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741		GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
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Db	1801		AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861		CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861		CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921		CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921		CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981		TTCTGCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981		TTCTGCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041		AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041		AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101		CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Db	2101		CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Qy	2161		AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161		AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221		ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280

Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
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Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
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Qy	2761	ATGATTTCGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
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Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCACT	2940
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Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
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Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
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Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
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Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
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Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
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Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
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Qy 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020  
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Qy 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCCATAAGTG 4080  
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 Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCCATAAGTG 4080

Qy 4081 TAAAATAAAAAGTTTACAGAAACCTT 4105  
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 Db 4081 TAAAATAAAAAGTTTACAGAAACCTT 4105

RESULT 5

HSET1R

LOCUS HSET1R 4105 bp mRNA linear PRI 23-MAR-1993

DEFINITION H.sapiens mRNA for endothelin-1 receptor.

ACCESSION X61950

VERSION X61950.1 GI:288312

KEYWORDS endothelin-1 receptor.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Hosoda,K., Nakao,K., Hiroshi-Arai, Suga,S., Ogawa,Y., Mukoyama,M.,  
 Shirakami,G., Saito,Y., Nakanishi,S. and Imura,H.

TITLE Cloning and expression of human endothelin-1 receptor cDNA

JOURNAL FEBS Lett. 287 (1-2), 23-26 (1991)

MEDLINE 91348221

PUBMED 1652463

FEATURES

source

Location/Qualifiers

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BASE COUNT 1138 a 859 c 845 g 1263 t

ORIGIN

Query Match 100.0%; Score 4105; DB 9; Length 4105;  
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Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCTCCGGAGTTTTCTTTTTCTGTGCGAGCCCT	120
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Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
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Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
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Qy	301	CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCCTC	360
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Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
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Qy	481	CAAGATGGAAACCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
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Qy	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCTGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCTGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACTGTGATATCTTGTAATATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACTGTGATATCTTGTAATATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900

Db	841	 AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	 GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	 GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	 TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	1021	 TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Qy	1081	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	 TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Db	1141	 TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Qy	1201	 TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	 TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
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Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580

Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
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Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
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Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
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ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Arai,H., Nakao,K., Hosoda,K., Ogawa,Y., Nakagawa,O., Komatsu,Y. and Imura,H.

TITLE Molecular cloning of human endothelin receptors and their expression in vascular endothelial cells and smooth muscle cells

JOURNAL Jpn. Circ. J. 56 Suppl 5, 1303-1307 (1992)

MEDLINE 93180293

PUBMED 1291713

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 128422] from the original journal article. This sequence comes from Fig. 5.

FEATURES

Location/Qualifiers

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BASE COUNT 1138 a 859 c 843 g 1263 t 2 others

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Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
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Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
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Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
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Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660

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 Db 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840

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Qy 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020  
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 Db 4081 TAAAATAAAAGTTTACAGAAACCTT 4105

# RESULT 7

HUMETN1R

LOCUS HUMETN1R 4101 bp mRNA linear PRI 18-DEC-2002

DEFINITION Homo sapiens mRNA for endothelin-1 receptor, complete cds.

ACCESSION D90348

VERSION D90348.1 GI:219649

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4101)

AUTHORS Hosoda,K., Nakao,K., Hiroshi-Arai, Suga,S., Ogawa,Y., Mukoyama,M.,  
 Shirakami,G., Saito,Y., Nakanishi,S. and Imura,H.

TITLE Cloning and expression of human endothelin-1 receptor cDNA

JOURNAL FEBS Lett. 287 (1-2), 23-26 (1991)

MEDLINE 91348221

PUBMED 1652463

COMMENT These data kindly submitted in computer readable form by: Kazuwa  
 Nakao

Second Division, Department of Medicine  
 Kyoto University School of Medicine  
 54 Shogoin Kawahara-cho

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FEATURES             Location/Qualifiers
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                        PEAIGFVMVPFEYRGEQHKTCMLNATSKFMEFYQDVKDWLFGFYFCMPLVCTAIFYT
                        LMTCEMLNRRNGSLRIALSEHLKQRREVAKTVFCLVVIFALCWFPPLHLSRI LKKT VYN
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BASE COUNT          1136 a      859 c      844 g      1262 t
ORIGIN

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Query Match 99.9%; Score 4101; DB 9; Length 4101;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	GGGGAGGACAGACTGGAGGCGTGTTCTCTCCGGAGTTTCTTTTTCTGTGCGAGCCCTCGCG	120
Qy	125	CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC	184
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Qy	245	TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA	304
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Qy	305	GCCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCCTCTGGC	364
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Qy	365	CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAA	424
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Qy	485	ATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	544
Db	481	ATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	540
Qy	545	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT	604
Db	541	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT	600
Qy	605	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	601	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	660
Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	724
Db	661	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	720
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	784
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Qy	785	CTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
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Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905	CTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
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Qy	965	TTCCCCCTTTTTCGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
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Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCTTTTG	1084
Db	1021	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCTTTTG	1080
Qy	1085	GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1144
Db	1081	GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1140
Qy	1145	GCGATTGGCTTCGTCTGTTACCCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	1141	GCGATTGGCTTCGTCTGTTACCCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
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Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCCTCATGACTTGT	1324
Db	1261	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	1321	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTC	1444
Db	1381	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTC	1440
Qy	1445	CCTCTTCACTTAAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	CCTCTTCACTTAAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATG	1564
Db	1501	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATG	1560
Qy	1565	AATTTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCACTCCAAAAGTCTGATGACCTCGGTCCCCATG	1684
Db	1621	CAGTCATGCCTCTGCTGCTGCTGTTACCACTCCAAAAGTCTGATGACCTCGGTCCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGAAGAAACCAAGATCAAAAACAACCACAACACAGACCGGAGC	1744
Db	1681	AACGGAACAAGCATCCAGTGAAGAAACCAAGATCAAAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAATC	1804
Db	1741	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAATC	1800
Qy	1805	CTCTCGGAGAAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	CTCTCGGAGAAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1924
Db	1861	TTCCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
Qy	1925	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1984
Db	1921	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTGTGATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	GCGTGTGTGATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGAT	2164

Db	2101	 CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2224
Db	2161	 TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2220
Qy	2225	GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2284
Db	2221	 GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATA	2344
Db	2281	 AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATA	2340
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Db	2341	 GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAACAC	2400
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Db	2401	 AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2524
Db	2461	 GCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2520
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Qy	2705	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATGA	2764
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Db	2761	 TTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2820
Qy	2825	TCCTATTCTCTTAATTTTTTGTTAAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2884
Db	2821	 TCCTATTCTCTTAATTTTTTGTTAAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2880
Qy	2885	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2944
Db	2881	 CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2940
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Db	2941	AATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTTCAG	3000
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Db	3001	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGCC	3060
Qy	3065	CACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3124
Db	3061	CACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3120
Qy	3125	TCTTTTACTAGTGTGTGTGTGTATATATATAACAATTGTAAATTTCTTTTAGCCCATTT	3184
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Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
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Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480
Qy	3485	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3544
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Db	3601	TGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3660
Qy	3665	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTACACCATTTTGTTTAGACAA	3844
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Qy      3845 TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTC 3904
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Db      4081 ATAAAAGTTTACAGAAACCTT 4101

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RESULT 8

AR270694

LOCUS AR270694 4079 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 1257 from patent US 6500938.

ACCESSION AR270694

VERSION AR270694.1 GI:29701928

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 4079)

AUTHORS Au-Young, J. and Seilhamer, J.J.

TITLE Composition for the detection of signaling pathway gene expression

JOURNAL Patent: US 6500938-A 1257 31-DEC-2002;

FEATURES Location/Qualifiers

source 1. 4079

/organism="unknown"

BASE COUNT 1125 a 856 c 842 g 1256 t

ORIGIN

Query Match 99.4%; Score 4079; DB 6; Length 4079;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	185	CATCCACCCCGGTTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG	244
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Qy	245	TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA	304
Db	241	TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA	300
Qy	305	GCCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTCTCCGGCTTCCTCTGGC	364
Db	301	GCCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTCTCCGGCTTCCTCTGGC	360
Qy	365	CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAA	424
Db	361	CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAA	420
Qy	425	AGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCTCAAG	484
Db	421	AGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCTCAAG	480
Qy	485	ATGGAAACCCTTTGCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	544
Db	481	ATGGAAACCCTTTGCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	540
Qy	545	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT	604
Db	541	GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT	600
Qy	605	CGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	601	CGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	660
Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAACTTCTCAGCTTTCAA	724
Db	661	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAACTTCTCAGCTTTCAA	720
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	784
Db	721	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	780
Qy	785	CTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	781	CTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	840
Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965	TTCCCCTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961	TTCCCCTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020

Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCTTTG	1084
Db	1021	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCTTTG	1080
Qy	1085	GTAAGTGCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1144
Db	1081	GTAAGTGCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1140
Qy	1145	GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTGTATG	1204
Db	1141	GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGACTTGT	1324
Db	1261	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	1321	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGTCTGGTTC	1444
Db	1381	CGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGTCTGGTTC	1440
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	CCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATG	1564
Db	1501	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1684
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Qy	1685	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1744
Db	1681	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATC	1804
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Qy	1805	CTCTCGGAGAAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	CTCTCGGAGAAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
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Db	1861	 TTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
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Qy	1985	GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	 GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	 GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGAT	2164
Db	2101	 CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2224
Db	2161	 TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2220
Qy	2225	GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2284
Db	2221	 GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAATA	2344
Db	2281	 AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAATA	2340
Qy	2345	GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAACAC	2404
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Qy	2405	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
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Qy	2645	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2704
Db	2641	 TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2700
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Db	2701	TGCACTGTATATAGAAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATGA	2760
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Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
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Qy	3245	TGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATAGTCT	3304
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Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
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# RESULT 9

S45956

LOCUS S45956 3305 bp mRNA linear PRI 08-MAY-1993

DEFINITION endothelin receptor subtype A [human, placenta, mRNA, 3305 nt].

ACCESSION S45956

VERSION S45956.1 GI:257375

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3305)

AUTHORS Hayzer,D.J., Rose,P.M., Lynch,J.S., Webb,M.L., Kienzle,B.K.,  
 Liu,E.C., Bogosian,E.A., Brinson,E. and Runge,M.S.

TITLE Cloning and expression of a human endothelin receptor: subtype A

JOURNAL Am. J. Med. Sci. 304 (4), 231-238 (1992)

MEDLINE 93035452

PUBMED 1415318

REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI gibbsq 115436] from the original journal article.

This sequence comes from Fig. 2.

FEATURES Location/Qualifiers

source 1..3305

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ORIGIN

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Qy	2122	GTGAATGTTCAATGGGAACTGGTCAACCATGAAACTTTTAGAGATTAACGACAAGATTTTCT	2181
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Qy	2182	ACTTTTTTTTAAGTGA - TTTTTTGTCCCTTCAGCCAAACACAATATGGGCTCAGGTCACTTT	2240
Db	1920	ACTTTTTTTTAAGTGATTTTTTTTTGGCCTTCAGCCAAACACAATATGGGCTCAAGTCACTTT	1979
Qy	2241	TATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTAT	2300
Db	1980	TATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTAT	2039
Qy	2301	TTGAACTTATTTACACATAGTTTGAAAAAAGACAAAAATAGTATTTCAGGTGAGCAA	2360
Db	2040	TTGAACTTATTTACACATAGTTTGAAAAAAGACAAAAATAGTATTTCAGGTGAGCAA	2099
Qy	2361	TTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAAAACACAAATTCCTAAAGCTACA	2420
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Qy	2421	ACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTTTAAATAGATGT	2480
Db	2160	ACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTTTAAATAGATGT	2219
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Db	2220	TACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGGTGTTTTATTACAAGGG	2279
Qy	2541	ACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCAATCAGATAGTTCTTTT	2600
Db	2280	ACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCAATCAGATAGTTCTTTT	2339
Qy	2601	TCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAATCAATGTCAAGTACCA	2660
Db	2340	TCACAAGTTCAAT-CTGTTTTTCATGTAAATTTTCGTATGAAAAATCAATGTCAAGTACCA	2398
Qy	2661	AAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTTCAGTGCAGTGTATATAGAA	2720
Db	2399	AAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTTCAGAGCACTGTATATAGAA	2458
Qy	2721	GTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATGATTCGGAAAATTTTCATT	2780
Db	2459	GTCTAAAACACACCTAAGAG-AAAAGATCGAATTTTTTCAGATGATTCAGAAAATTTTCATT	2517
Qy	2781	CAGGTATTTGTAATAGTGACATATATATGTATATACATATCACCTCCTATTCTCTTAATT	2840
Db	2518	CAGGTATTTGGAATAGTGACATATATATGTATATACATATCACCTCCTATTCTCTTAATT	2577
Qy	2841	TTTGTTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCCTTTTCCATATAGGAA	2900
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Qy	2901	ACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAATTACCCACAAA	2960
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Qy	2961	TGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTTCAGTATGAACCTAACTCCC	3020
Db	2698	TGCCACCAG--AACTTACGATTCTTCACTTCTTGGGGTTTTTCAGTATGAACCTAACTCCC	2755
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Db	2876	GTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATTTTCTAGACTGTCTCTG	2935
Qy	3201	TGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTATGTATGGATTTAATCT	3260
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Qy      3441 TGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGTATAAAGCAGTATT 3500
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Qy      3501 TGGGGTCATATTGTTTTCCTGTGCTGGAGCAAAAGTCATTACACTTTGAAGTATTATATTG 3560
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Qy      3561 TTCTTATCCT 3570
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# RESULT 10

BC022511

LOCUS BC022511 2705 bp mRNA linear PRI 04-FEB-2002

DEFINITION Homo sapiens, endothelin receptor type A, clone MGC:26548

IMAGE:4812050, mRNA, complete cds.

ACCESSION BC022511

VERSION BC022511.1 GI:18490297

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2705)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 32 Row: j Column: 7  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503464.

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                        /mol_type="mRNA"
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                        /db_xref="taxon:9606"
                        /clone="MGC:26548 IMAGE:4812050"
                        /tissue_type="Brain, hippocampus"
                        /clone_lib="NIH_MGC_95"
                        /lab_host="DH10B"
                        /note="Vector: pBluescript"
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                        /protein_id="AAH22511.1"
                        /db_xref="GI:18490298"
                        /translation="METLCLRASFWLALVGCVISDNPERYSTNLSNHVDDFTTFRGTE
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PEAIGFVMVPFEYRGEQHKTCMLNATSKFMEFYQDVKDWLFGFYFCMPLVCTAIFYT
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BASE COUNT           767 a    594 c    560 g    784 t
ORIGIN
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Query Match 63.6%; Score 2609.6; DB 9; Length 2705;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2673; Conservative 0; Mismatches 14; Indels 5; Gaps 5;

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Qy      194 CGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAGTGCCAGGA 253
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Qy      254 AGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGCCGAGCCCGGGAC 313
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Qy      314 ACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGCCCAGGCGCC 373
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Qy      374 GCGCGGACCCGGCAGCTGTCTGCGCAGCCGAGCTCCACGGTGAAAAAAAAAAGTGAAGGT 433
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Qy	614		GAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCCAGCAATGGC	673
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Qy	674		TCAATGCACAACACTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAAC	733
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Qy	734		ACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGG	793
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Qy	794		ATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCC	853
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Qy	854		CTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCT	913
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Qy	914		GGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTT	973
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Qy	974		TTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGG	1033
Db	840		TTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGG	899
Qy	1034		TACAGAGCAGTTGCCTCCTGGAGTCGTGTTTACGGGAATTGGGATTCTTTGGTAACTGCC	1093
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Qy	1094		ATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGC	1153
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Db	1020		TTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC	1079
Qy	1214		ACATCAAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTAT	1273
Db	1080		ACATCAAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTAT	1139
Qy	1274		TTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTG	1333

Db	1140	TTCTGTATGCCCTTGGTGTGCACTGCCATCTTCTACACCCCTCATGACTTGTGAGATGTTG	1199
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Db	1200	AACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAA	1259
Qy	1394	GTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCAC	1453
Db	1260	GTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTGTTTCAT	1319
Qy	1454	TTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTA	1513
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Qy	1514	CTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATGAATTCATGT	1573
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Qy	1634	CTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATGAACGGAAACA	1693
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Qy	1694	AGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGCAGCCATAAG	1753
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Qy	1874	TCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCA	1932
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# RESULT 11

BD169895

LOCUS BD169895 2595 bp DNA linear PAT 17-JAN-2003  
 DEFINITION Method for examination of allergosis.  
 ACCESSION BD169895  
 VERSION BD169895.1 GI:27875707  
 KEYWORDS WO 02052006-A/28.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2595)  
AUTHORS Otani,N., Matsui,K., Yoshida,N., Sugita,Y. and Izuhara,K.  
TITLE Method for examination of allergosis  
JOURNAL Patent: WO 02052006-A 28 04-JUL-2002;  
GENOX RESEARCH INC,NORIKO OTANI,KEIKO MATSUI,NEI YOSHIDA, YUJI  
SUGITA, KENJI IZUHARA  
COMMENT OS Homo sapiens (human)  
PN WO 02052006-A/28  
PD 04-JUL-2002  
PF 21-DEC-2001 WO 2001JP011287  
PR 26-DEC-2000 JP 00P 396166  
PI NORIKO OTANI,KEIKO MATSUI,NEI YOSHIDA,YUJI SUGITA,KENJI PI  
IZUHARA  
PC C12N15/12,C12Q1/68,C12Q1/02,A01K67/027,A61K31/713,A61K45/00,  
PC A61K48/00,  
PC A61P37/08,G01N33/15,G01N33/50,G01N33/53  
CC Method for examination of allergosis  
FH Key Location/Qualifiers  
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Db 255 CTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG 314  
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Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGA	2163
Db	495	 GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	 TTAACGACAAGATTTTCTACTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
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Db	675	 TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAACA	2403
Db	735	 AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	 CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	 GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	2583
Db	915	 GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	 AATCAGATAGTTCTTTTTTACAAGTTCAAT-CTGTTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	 ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	 GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	 ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTTGTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883

Db	1214	CTCCTATTCTCTTAATTTTTGTGTTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
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Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTTCACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113

Qy 3724 GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT 3783  
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 Db 2114 GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT 2173  
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 Db 2174 CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTACACCATTTTGTTTAGACA 2233  
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 Db 2234 ATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT 2293  
 Qy 3904 CAGAAAGTCATAGATTTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 3963  
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 Db 2294 CAGAAAGTCATAGATTTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 2353  
 Qy 3964 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 4023  
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 Db 2354 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 2413  
 Qy 4024 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTA 4083  
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 Db 2414 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTA 2473  
 Qy 4084 AATAAAAGTTTACAGAAACCTT 4105  
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 Db 2474 AATAAAAGTTTACAGAAACCTT 2495

# RESULT 12

D11144S8

LOCUS D11144S8 2595 bp DNA linear PRI 19-SEP-2002

DEFINITION Homo sapiens gene for endothelin-A receptor, complete cds, exon 8 and 3' flanking region.

ACCESSION D11151

VERSION D11151.1 GI:219628

KEYWORDS G protein-coupled receptor; endothelium; smooth muscle.

SEGMENT 8 of 8

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2595)

AUTHORS Hosoda,K., Nakao,K., Tamura,N., Arai,H., Ogawa,Y., Suga,S., Nakanishi,S. and Imura,H.

TITLE Organization, structure, chromosomal assignment, and expression of the gene encoding the human endothelin-A receptor

JOURNAL J. Biol. Chem. 267 (26), 18797-18804 (1992)

MEDLINE 92406798

PUBMED 1326535

REFERENCE 2 (bases 1 to 2595)

AUTHORS Hosoda,K.

TITLE Direct Submission

JOURNAL Submitted (18-MAY-1992) Kiminori Hosoda, Kyoto University School of Medicine, Department of Medicine; 54 Shogoin Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan (Tel:81-75-751-3170,

Fax:81-75-771-9452)

FEATURES                      Location/Qualifiers  
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BASE COUNT            788 a        478 c        459 g        870 t  
ORIGIN

Query Match                      60.2%;    Score 2470;    DB 9;    Length 2595;  
Best Local Similarity    100.0%;    Pred. No. 0;  
Matches 2481;    Conservative    0;    Mismatches    0;    Indels    1;    Gaps    1;

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QY	1684	GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG	1743
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QY	1744	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1803
Db	135	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	194
QY	1804	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	1863
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QY	1864	CTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	1923
Db	255	CTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	314
QY	1924	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	1983



Db	315	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	374
Qy	1984	TGCGTGTGTGATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	2043
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Qy	2044	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAGTACATGGCTA	2103
Db	435	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAGTACATGGCTA	494
Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	2163
Db	495	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
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Qy	2224	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTTAAATG	2523
Db	855	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTTAAATG	914
Qy	2524	GTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	2583
Db	915	GTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTCAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTAACCTGCGCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTAACCTGCGCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213

Qy	2824	CTCCTATTCTCTTAATTTTGTGTTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATT	2883
Db	1214	CTCCTATTCTCTTAATTTTGTGTTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATT	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
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Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
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Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053

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 Db 2474 AATAAAAGTTTACAGAAACCTT 2495

# RESULT 13

AC093908

LOCUS AC093908 164920 bp DNA linear PRI 01-MAR-2002

DEFINITION Homo sapiens BAC clone RP11-752L20 from 4, complete sequence.

ACCESSION AC093908 AC067873

VERSION AC093908.3 GI:18497272

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 164920)

AUTHORS Sulston,J.E. and Waterston,R.

TITLE Toward a complete human genome sequence

JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE 99063792

PUBMED 9847074

REFERENCE 2 (bases 1 to 164920)

AUTHORS Paulson,E., Cotton,M. and Creason,K.

TITLE The sequence of Homo sapiens BAC clone RP11-752L20

JOURNAL Unpublished (2001)

REFERENCE 3 (bases 1 to 164920)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 164920)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (05-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 164920)

AUTHORS Waterston,R.

TITLE Direct Submission

JOURNAL Submitted (08-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 6 (bases 1 to 164920)

AUTHORS Waterston,R.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT On Feb 5, 2002 this sequence version replaced gi:15778805.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: [sapiens@watson.wustl.edu](mailto:sapiens@watson.wustl.edu)

----- Summary Statistics

Center project name: H\_NH0752L20

Drafting Center: WIBR

-----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

#### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-56F3. Actual start of this clone is at base position 1 of RP11-752L20; actual end is at base position 164920 of RP11-752L20.

Data from AC083898 was used to finish this clone, AC093908.

The sequence of AC067873 has been incorporated into AC093908.

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repeat_region	323. .393 /rpt_family="L1"
repeat_region	4328. .4359 /rpt_family="AT_rich"
repeat_region	4786. .4811 /rpt_family="(CA)n"
repeat_region	4813. .4874 /rpt_family="(TC)n"
repeat_region	4883. .4910 /rpt_family="(CA)n"
repeat_region	4948. .5511 /rpt_family="L1"
repeat_region	5058. .5099 /rpt_family="AT_rich"
repeat_region	5129. .5164 /rpt_family="AT_rich"
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repeat_region	6126. .6196 /rpt_family="MER1_type"
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Best Local Similarity 99.4%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 8; Indels 6; Gaps 5;

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Qy	3482	GGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTAC	3541
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Db	95634	TTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGT	95693
Qy	3962	AACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAA	4021
Db	95694	AACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAA	95753

Qy 4022 GTAAC TTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGT 4081  
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 Db 95754 GTAAC TTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGT 95813  
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RESULT 14

G06463

LOCUS G06463 2337 bp DNA linear STS 19-OCT-1995

DEFINITION human STS WI-7226, sequence tagged site.

ACCESSION G06463

VERSION G06463.1 GI:859708

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2337)

AUTHORS Hudson,T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
 Mapped ESTs

JOURNAL Unpublished (1995)

COMMENT

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 Whitehead Institute/MIT Center for Genome Research  
 Whitehead Institute for Biomedical Research  
 9 Cambridge Center, Cambridge MA 02142 USA  
 Tel: 617 252 1900  
 Fax: 617 252 1902  
 Email: thudson@genome.wi.mit.edu

Primer A: GATCGAATTTTTCAGATGATTCTG

Primer B: AAATGCCCAGCAAAAGTCAC

STS size: 343

PCR Profile:

Presoak:  
 Denaturation:  
 Annealing: 56 degrees C  
 Polymerization:  
 PCR Cycles: 35  
 Thermal Cycler:

Protocol:

Template: 10 ng  
 Primer: each 5 pM  
 dNTPs: each 4 nM  
 Taq Polymerase: 0.025 units/ul  
 Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM  
 KCl: 50 mM  
 Tris-HCL: 10 mM  
 pH: 9.3

Prepared with primer pairs derived from D90348 -- Unigene.

FEATURES                      Location/Qualifiers  
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    primer\_bind              complement(1301. .1320)  
BASE COUNT            694 a      407 c      407 g      784 t      45 others  
ORIGIN

Query Match                      55.8%;    Score 2292;    DB 11;    Length 2337;  
Best Local Similarity    98.1%;    Pred. No. 0;  
Matches 2292;    Conservative    0;    Mismatches    45;    Indels      0;    Gaps      0;

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Db	121	AGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGGTTTATCCACCCACAACATCTACGA	180
Qy	1949	ATCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCACTAAAAA	2008
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Qy	2069	TTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATG	2128
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Qy	2189	TTAAGTGATTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACTTTTATTTGAA	2248
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Qy	2249	ATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACTT	2308
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Db	601	GTATTTTCCACGTCACTATTTATTTTTTTTAAAAACAAATTCTAAAGCTACAACAAATAC	660
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Qy	2729	CACACCTAAGAGAAAAAGATCGAATTTTTTCAGATGATTCGAAATTTTCATTCAGGTATT	2788
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Qy	2969	GTAACCTAACGATTCTTCACTTCTTGGGGTTTTTCAGTATGAACCTAACTCCCCACCCAA	3028
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Qy	3029	CATCTCCCTCCACATTGTCACCATTTCAAAGGGCCACAGTGACTTTTGCTGGGCATTT	3088
Db	1261	CATCTCCCTCCACATTGTCACCATTTCAAAGGGCCACAGTGACTTTTGCTGGGCATTT	1320
Qy	3089	TCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAATCTTTTACTAGTGTGTGTGTAT	3148
Db	1321	TCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAATCTTTTACTAGTGTGTGTGTAT	1380
Qy	3149	ATATATAAACAAATTGTAAATTTCTTTTAGCCCATTTTCTAGACTGTCTCTGTGGAATAT	3208
Db	1381	ATATATAAACAAATTGTAAATTTCTTTTAGCCCATTTTCTAGACTGTCTCTGTGGAATAT	1440

Qy	3209	ATTTGTGTGTGTGATATATGCATGTGTGTGATGGTATGTATGGATTTAATCTAATCTAAT	3268
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Qy	3269	AATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTCTGAGCTAAAATCTAGGTGATTGTTC	3328
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Qy	3389	TGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGT	3448
Db	1621	TGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGT	1680
Qy	3449	GGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTATTTGGGGTCA	3508
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Qy	3569	CTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTTCAGACTTCGCCA	3628
Db	1801	CTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTTCAGACTTCGCCA	1860
Qy	3629	GACAGATTGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGT	3688
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Qy	3689	AAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTG	3748
Db	1921	AAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTG	1980
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Db	1981	TGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAA	2040
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Db	2041	TATAAGCCATAGGTTACACCATTTTGTTTAGACAATTGTCTTTTTTTCAAGATGCTTTG	2100
Qy	3869	TTTCTTTTCATATGAAAAAATGCATTTTATAAATTCAGAAAGTCATAGATTTCTGAAGGC	3928
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Query Match 44.3%; Score 1819.6; DB 9; Length 1868;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Qy 2160 GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA 2218  
|||||  
Db 1750 GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTTGTCTTCAGCCAAACA 1809  
Qy 2219 CAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT 2268  
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Db 1810 CAATATGGGCTCAAGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT 1859

Search completed: December 12, 2003, 19:39:03  
Job time : 14421.7 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:17:01 ; Search time 7395.45 Seconds  
(without alignments)  
13490.718 Million cell updates/sec

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Perfect score: 4105  
Sequence: 1 gaattcgcgccgcctcttg.....taaaagtttacagaaacctt 4105

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
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5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
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19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	%		Query			Description
	No.	Score	Match	Length	ID	
	1	1069	26.0	3538	11 AK043210	AK043210 Mus muscu
	2	797.8	19.4	865	9 AU118882	AU118882 AU118882
	3	792.2	19.3	863	9 AU119546	AU119546 AU119546
	4	789	19.2	869	9 AU120519	AU120519 AU120519
	5	752.2	18.3	783	13 BX109539	BX109539 BX109539
	6	750.6	18.3	3150	11 AK042211	AK042211 Mus muscu
c	7	725.6	17.7	781	9 AI936539	AI936539 wd29b09.x
	8	710.4	17.3	733	12 BM719244	BM719244 UI-E-EO1-
c	9	704.2	17.2	777	12 BQ018994	BQ018994 UI-H-DH1-
	10	695.8	17.0	764	9 AU139639	AU139639 AU139639
	11	694.8	16.9	782	14 CD246193	CD246193 AGENCOURT
c	12	694.4	16.9	739	9 AI694278	AI694278 wd45a01.x
c	13	692.2	16.9	732	13 BQ575745	BQ575745 UI-H-EZ1-
c	14	687.8	16.8	747	9 AI809396	AI809396 wf70b01.x
c	15	685	16.7	705	12 BQ006584	BQ006584 UI-H-EI1-
	16	683	16.6	742	10 BG116534	BG116534 602317635
	17	683	16.6	771	10 BG699589	BG699589 602679314
c	18	681.4	16.6	703	13 BU681421	BU681421 UI-CF-EC1
c	19	673	16.4	677	9 AI130721	AI130721 qc16e12.x
c	20	661	16.1	661	13 BU948045	BU948045 io49d10.x
c	21	653.4	15.9	724	9 AI953824	AI953824 wx69h09.x
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c	24	647.6	15.8	679	13 BU687640	BU687640 UI-CF-EC1
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c	27	621.6	15.1	678	9 AI804414	AI804414 tc71a03.x
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## ALIGNMENTS

## RESULT 1

AK043210

LOCUS AK043210 3538 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730071B21 product:SIMILAR TO ENDOTHELIN RECEPTOR TYPE A, full insert sequence.

ACCESSION AK043210

VERSION AK043210.1 GI:26335584

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

## REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,  
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,  
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,  
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,  
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,  
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,  
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.  
and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409 (6821), 685-690 (2001)  
MEDLINE 21085660  
PUBMED 11217851  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE 6 (bases 1 to 3538)  
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,  
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,  
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers  
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CDS

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ORIGIN

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Db	565	ATATCCTGCACCATTTTCATCGTGGGAATGGTGGGGAACGCAACTCTACTACGAATCATT	624
Qy	800	TACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGA	859
Db	625	TACCAAAACAAGTGTATGAGGAACGGCCCCAATGCGCTCATAGCCAGCCTGGCCCTTGGA	684
Qy	860	GACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGC	919
Db	685	GACCTTATCTACGTGGTCATTGACCTCCCCATCAACGTGTTTAAGCTCTTGGCAGGACGC	744
Qy	920	TGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAG	979
Db	745	TGGCCTTTTCGACCACAATGATTTTGGAGTGTTTCTCTGCAAGCTGTTCCCCTTCCTGCAG	804
Qy	980	AAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGA	1039
Db	805	AAGTCCTCCGTGGGCATCACCGTCTTGAACCTCTGTGCTCTCAGTGTGGACAGGTACAGA	864
Qy	1040	GCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATGGGATTCCTTTGGTAACTGCCATTGAA	1099
Db	865	GCAGTGGCTTCCTGGAGCCGAGTTCAAGGAATCGGGATCCCCTTGATTACCGCCATTGAA	924
Qy	1100	ATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTC	1159
Db	925	ATCGTCTCCATCTGGATTCTTTCCTTCATCTTGGCCATCCCGGAAGCAATCGGCTTCGTC	984
Qy	1160	ATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCCACATCA	1219
Db	985	ATGGTACCCTTCGAATACAAGGGCGAGCTGCATAGGACCTGCATGCTCAACGCCACGTCC	1044
Qy	1220	AAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGT	1279
Db	1045	AAGTTTCATGGAGTTTTACCAAGATGTGAAGGACTGGTGGCTCTTGGGTTCTACTTCTGC	1104
Qy	1280	ATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGA	1339
Db	1105	ATGCCCTTGGTGTGACAGCAATCTTCTACACCCTCATGACCTGTGAGATGCTCAACAGG	1164
Qy	1340	AGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCA	1399
Db	1165	AGGAACGGCAGCTTGCGGATCGCCCTTAGTGAGCACCTCAAACAGCGTCGAGAAGTGGCA	1224
Qy	1400	AAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTCCCTCTTCACTTAAGC	1459
Db	1225	AAGACTGTCTTCTGCTTGGTTGTCATCTTCGCCCTGTGCTGGTTCCCTCTTCACTTAAGC	1284
Qy	1460	CGTATATTGAAGAAAACGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGT	1519





Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 865)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished

COMMENT Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genomics@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES Location/Qualifiers

source 1. .865  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HEMBA1004569"  
/tissue\_type="whole embryo, mainly head"  
/dev\_stage="embryo, 10 weeks"  
/clone\_lib="HEMBA1"  
/note="Vector: pME18SFL3"

BASE COUNT 271 a 184 c 158 g 247 t 5 others

ORIGIN

Query Match 19.4%; Score 797.8; DB 9; Length 865;  
Best Local Similarity 98.0%; Pred. No. 6.1e-145;  
Matches 847; Conservative 0; Mismatches 12; Indels 5; Gaps 4;

Qy 1479 TGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATT 1538  
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Db 1 TGNATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATT 60

Qy 1539 ACATCGGTATTAACTTGGCAACCATGAATTTCATGTATAAACCCCATAGCTCTGTATTTTG 1598  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 61 ACATCGGTATTAACTTGGCAACCATGAATTTCATGTATAAACCCCATAGCTCTGTATTTTG 120

Qy 1599 TGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCA 1658  
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Db 121 TGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCA 180

Qy 1659 AAAGTCTGATGACCTCGGTCCCCATGAACGGAACAAGCATCCAGTGGAAGAACCACGATC 1718  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 181 AAAGTCTGATGACCTCGGTCCCCATGAACGGAACAAGCATCCAGTGGAAGAACCACGATC 240

Qy 1719 AAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAG 1778  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 241 AAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAG 300

Qy 1779 AAGCACTCCTCGGTACTCCCATATCTCTCGGAGAAAAAATCACAAGGCAACTGTGAC 1838

```

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Db      301 AAGCACTCCTCGGTACTCCATAATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAG 360
Qy      1839 TCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCCTCCACACCCAAGAAGAAATG 1898
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Db      361 TCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCCTCCACACCCAAGAAGAAATG 420
Qy      1899 CTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCACCCACAACATCTACGAATCGTACTT 1957
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Db      421 CTTTCCAAAACCGCAAGGGTAGACTGGTTTATCCACCCACAACATCTACGAATCGTACTT 480
Qy      1958 CTTTAATTGATCTAATTTACATATTCTGCGTGTGTATTTCAGCACTAAAAAATGGTGGA 2017
      |||
Db      481 CTTTAATTGATCTAATTTACATATTCTGCGTGTGTATTTCAGCACTAAAAAATGGTGGA 540
Qy      2018 GCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGCATGA 2077
      |||
Db      541 GCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGCATGA 600
Qy      2078 AAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGG 2137
      |||
Db      601 AAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGG 660
Qy      2138 AACTGGTCACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTAAGTGA- 2196
      |||
Db      661 AACTGGTCACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTAAGTGAT 720
Qy      2197 TTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATT 2256
      |||
Db      721 TTTTTTGNCTTCAGCCAAACACAATATGGGCTCAAGTCACTTTTATTTGAAATGNCATT 780
Qy      2257 TGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATG--ATTATTTGAACTTATTTA- 2313
      |||
Db      781 TGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGGATTATTTGGAACCTTATTTAC 840
Qy      2314 CACATAGTTTGAAAAAAAAAAGAC 2337
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Db      841 CNCNTAGTTTGAAAAAAAAAAGAC 864

```

# RESULT 3

AU119546

LOCUS AU119546 863 bp mRNA linear EST 01-AUG-2002

DEFINITION AU119546 HEMBA1 Homo sapiens cDNA clone HEMBA1006071 5', mRNA sequence.

ACCESSION AU119546

VERSION AU119546.1 GI:10934781

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 863)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project



Qy	2463	TGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAAT	2522
Db	420	TGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAAT	479
Qy	2523	GGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTT	2582
Db	480	GGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTT	539
Qy	2583	CAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAA	2642
Db	540	CAATCAGATAGTTCTTTTTCAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAA	598
Qy	2643	AATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTC	2702
Db	599	AATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTC	658
Qy	2703	AGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGAT	2762
Db	659	AGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGAT	718
Qy	2763	GATTTCGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCA	2822
Db	719	GATTTCGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGNATATACATATCA	778
Qy	2823	CCTCCTATTCTCTTAATTTTGTAAAAATGTTAACTGGCAGT-AAGTCTTTTGTATCAT	2881
Db	779	CCTCCTATTCTCTTAATTTTCTTAAAAATGGTAACTGGCAGTAAAGCCTTTTGTACCAT	838
Qy	2882	TCCCTTTTCCATATAGGAAACATA	2905
Db	839	TCCCTTTTCATTTAGGGAAACTTA	862

#### RESULT 4

AU120519

LOCUS AU120519 869 bp mRNA linear EST 01-AUG-2002

DEFINITION AU120519 HEMBB1 Homo sapiens cDNA clone HEMBB1000846 5', mRNA sequence.

ACCESSION AU120519

VERSION AU120519.1 GI:10935754

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 869)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished

COMMENT Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986

Email: genomics@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix  
Research Institute; cDNA library construction: Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

FEATURES                      Location/Qualifiers  
    source                      1. .869  
                                /organism="Homo sapiens"  
                                /mol\_type="mRNA"  
                                /db\_xref="taxon:9606"  
                                /clone="HEM BB1000846"  
                                /tissue\_type="whole embryo, mainly body"  
                                /dev\_stage="embryo, 10 weeks"  
                                /clone\_lib="HEM BB1"  
                                /note="Vector: pME18SFL3"  
BASE COUNT                      277 a       153 c       148 g       289 t           2 others  
ORIGIN

Query Match                      19.2%;   Score 789;   DB 9;   Length 869;  
Best Local Similarity           98.0%;   Pred. No. 3.2e-143;  
Matches 850;   Conservative       0;   Mismatches   12;   Indels       5;   Gaps       5;

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Qy      1771 ACCCTTAGAAGCACTCCTCGGTACTCCATAATCCTCTCGGAGAAAAAATCA CAAGGCA 1830
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Db      1 ACCCTTAGAAGCACTCCTCGGTACTCCATAATCCTCTCGGAGAAAAAATCA CAAGGCA 60

Qy      1831 ACTGTGACTCCGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACTCCCAACCCAAG 1890
          |||
Db      61 ACTGTGAGTCCGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACTCCCAACCCAAG 120

Qy      1891 AAGAAATGCTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCACCCACAACATCTACGAA 1949
          |||
Db      121 AAGAAATGCTTTCCAAAACCGCAAGGTAGACTGGTTTATCCACCCACAACATCTACGAA 180

Qy      1950 TCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATT CAGCACTAAAAAA 2009
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Db      181 TCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATT CAGCACTAAAAAA 240

Qy      2010 TGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTT 2069
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Db      241 TGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTT 300

Qy      2070 TTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGT 2129
          |||
Db      301 TTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGT 360

Qy      2130 TCAATGGGAAGCTGGTCACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTT 2189
          |||
Db      361 TCAATGGGAAGCTGGTCACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTT 420

Qy      2190 TAAGTGA-TTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACTTTTATTTGAA 2248
          |||
Db      421 TAAGTGATTTTTTTGTCTTCAGCCAAACACAATATGGGCTCAAGTCACTTTTATTTGAA 480

Qy      2249 ATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACTT 2308
          |||
Db      481 ATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACTT 540
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Qy 2309 ATTTACACATAGTTTGAACAAAAAAGACAAAAATAGTATTTCAGGTGAGCAATTAGATTA 2368  
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 Db 541 ATTTACACATAGTTTGAACAAAAAAGACAAAAATAGTATTTCAGGTGAGCAATTAGATTA 600

Qy 2369 GTATTTTCCACGTCACTATTTATTTTAAAAACACAAATTCTAAAGCTACAACAAATAC 2428  
 |||  
 Db 601 GTATTTTCCACGTCACTGGTTATTTTAAAAACACANATTCTAAAGCTACAACAAATAC 660

Qy 2429 TACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAA 2488  
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 Db 661 TACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAA 720

Qy 2489 GAATTTTAAAGAACTGTATTTTATTTTAAATGGTGTATTATTACAAGGGACCTTGAA 2548  
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 Db 721 GAATTTTAAAGAACTGNATTTTATTTTGAATGGTGTATTATTACAAGGGACCTTG-A 779

Qy 2549 CATGTTTTGTATGTTAAATTCAAAGTAATGCTTCAATCAGATAGTTCTTTTTCACAAGT 2608  
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 Db 780 CATGTTTTGGATGGTAAATTCAAAGTAATGCTTCAATCAGATAGTTC-TTTTTCACAAGT 838

Qy 2609 TCAATACTGTTTTTCATGTAAATTTTG 2635  
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 Db 839 TCAAT-CTGGTTTTTCATGTAAATTTGG 864

# RESULT 5

BX109539

LOCUS BX109539 783 bp mRNA linear EST 07-FEB-2003

DEFINITION BX109539 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone  
 IMAGp998G221159 ; IMAGE:487341, mRNA sequence.

ACCESSION BX109539

VERSION BX109539.1 GI:27877774

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 783)

AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
 Radelof,U., Schneider,D. and Korn,B.

TITLE Human UnigeneSet - RZPD3

JOURNAL Unpublished

COMMENT Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGp998G221159.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human UnigeneSet - RZPD3 (RZPDLIB No.972)

[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972)

[bin/showLib.pl.cgi/response?libNo=972](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972) Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

[www.rzpd.de](http://www.rzpd.de)

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.

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FEATURES
    source          Location/Qualifiers
                    1. .783
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                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGp998G221159 ; IMAGE:487341"
                    /sex="female"
                    /dev_stage="adult"
                    /lab_host="DH10B"
                    /clone_lib="Soares_pregnant_uterus_NbHPU"
                    /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
                    Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                    oligo(dT) primer [5'
                    AACTGGAAGAATTTCGCGCCGCCTTTTTTTTTTTTTTTTTTTT 3'],
                    double-stranded cDNA was ligated to Eco RI adaptors
                    (Pharmacia), digested with Not I and cloned into the Not I
                    and Eco RI sites of the modified pT7T3 vector. Library
                    went through one round of normalization. Library
                    constructed by M. Fatima Bonaldo."
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BASE COUNT      217 a      139 c      155 g      269 t      3 others
ORIGIN
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Query Match          18.3%; Score 752.2; DB 13; Length 783;
Best Local Similarity 98.9%; Pred. No. 4.7e-136;
Matches 777; Conservative 0; Mismatches 6; Indels 3; Gaps 2;
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Qy      2899 AAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAATTACCCACA 2958
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Qy      2959 AATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCAGTATGAACCTAACTC 3018
          |||
Db      61 AATGCCACCAG--AACTTACGATTCTTCACTTCTTGGGGTTTTCAGTATGAACCTAACTC 118

Qy      3019 CCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGCCACAGTGACTTTTG 3078
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Db      119 CCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGCCACAGTGACTTTTG 178

Qy      3079 CTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAAATCTTTTACTAGTGT 3138
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Db      179 CTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAAATCTTTTACTAGTGT 238

Qy      3139 GTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATTTTCTAGACTGTCTC 3198
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Db      239 GTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATTTTCTAGACTGTCTC 298

Qy      3199 TGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTATGTATGGATTTAAT 3258
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Db      299 TGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTATGTATGGATTTAAT 358

Qy      3259 CTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCAATAGTCTGAGCTAAAATCTAG 3318
          |||
Db      359 CTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCAATAGTCTGAG-TAAAATCTAG 417

Qy      3319 GTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTAGCAACCTTCTGCAT 3378
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Db      418 GTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTAGCAACCTTCTGCAT 477
Qy      3379 TCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCA 3438
      |||
Db      478 TCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCA 537
Qy      3439 GATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTA 3498
      |||
Db      538 GATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTA 597
Qy      3499 TTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTTGAAGTATTATAT 3558
      |||
Db      598 TTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTTGAAGTATTATAT 657
Qy      3559 TGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCA 3618
      |||
Db      658 TGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCA 717
Qy      3619 GACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTT 3678
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Db      718 GACTTCGCCAGACAGATTGCTGATAATAAATTANGTAAGATAATTTGNTGGGCCATATTT 777
Qy      3679 TAGGAC 3684
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Db      778 TANGAC 783

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# RESULT 6

AK042211

LOCUS AK042211 3150 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630071G03 product:SIMILAR TO ENDOTHELIN RECEPTOR TYPE A, full insert sequence.

ACCESSION AK042211

VERSION AK042211.1 GI:26088888

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,



Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3150)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome



Qy	322	CCCTCCGCGCCACCCACCTCGCTTCTCCGGCTTCTCTGCGCCAGGCGCCGCGGGAC	381
Db	286	CCCTGCGCGCCACCCCTCGTTCCTCCAGCTCAGGCTCCGGCTGGCCCGTGCGC-----GGA	339
Qy	382	CCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAAAAGTGAAGGTGTAAAAGC	441
Db	340	CCTGGAGCTGTCTGCTTCCGAGGAGCTCTAAGGTGAAAAAAGAAAGGCGTGAGACCAAC	399
Qy	442	AGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAGATGGAAACCCTTTGCCT	501
Db	400	ATAAGAAG-----ACTTAAATCCAGGTTAAGATGAGTATCTTTTGCCT	443
Qy	502	CAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGTGATAATCCTGAGAGATA	561
Db	444	TGCGGCATACTTTTGGCTGACCATGGTGGGAGGCGTAATGGCTGACAATCCGGAGAGATA	503
Qy	562	CAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCACTTTTCGTGGCACAGAGCTCAG	621
Db	504	CAGCGCTAATCTAAGCAGCCACATGGAAGACTTCAACCCCTTTTCCGGGGACGGAGATCAA	563
Qy	622	CTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCCAGCAATGGCTCAATGCA	681
Db	564	CTTTCTGGGCACCACCCATCGACCCCTAATTTGGCCCTGCCTAGCAATGGCTCAATGCA	623
Qy	682	CAACTATTGCCCACAGCAGACTAAAAATTACTTCAGCTTTCAAATACATTAACTGTGAT	741
Db	624	CGGCTATTGCCCACAGCAGACTAAAAATCACGACAGCTTTCAAATATATTAACACTGTGAT	683
Qy	742	ATCTTGTAATAATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTA	801
Db	684	ATCCTGCACCAATTTTCATCGTGGGAATGGTGGGGAACGCAACTCTACTACGAATCATTTA	743
Qy	802	CCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGA	861
Db	744	CCAAAACAAGTGATGAGGAACGGCCCCAATGCGCTCATAGCCAGCCTGGCCCTTGGAGA	803
Qy	862	CCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTG	921
Db	804	CCTTATCTACGTGGTCATTGACCTCCCCATCAACGTGTTTAAGCTCTTGGCAGGACGCTG	863
Qy	922	GCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCAGAA	981
Db	864	GCCTTTTCGACCACAATGATTTTGGAGTGTTTCTCTGCAAGCTGTTCCCTTCTGCAGAA	923
Qy	982	GTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGC	1041
Db	924	GTCCTCCGTGGGCATCACCGTCTTGAACCTCTGTGCTCTCAGTGTGGACAGGTACAGAGC	983
Qy	1042	AGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAAT	1101
Db	984	AGTGGCTTCTCGGAGCCGAGTTCAAGGAATCGGGATCCCCTTGATTACCGCCATTGAAAT	1043
Qy	1102	TGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCAT	1161
Db	1044	CGTCTCCATCTGGATTCTTTCTTCATCTTGGCCATCCCGGAAGCAATCGGCTTCGTCAT	1103



BASE COUNT	264 a	154 c	129 g	232 t	2 others
ORIGIN					

Qy	3336	CAACCTGCCTCAGTCCATTTTAAACCTGTAGCAACCTTCTGCATTTCATAAAATCTTGTAAATC	3395
Db	773	CAAACAGCTTCAGTCCATTTT-ACCTGTAGCAACCGTCTGCATTTCATAATTCTTGTAGTC	715
Qy	3396	ATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAG	3455
Db	714	ATGTACCCATTACNAATGGGATATAAGAGCAAGCGTGAAAGCAGATGAGCTGTGACTAAG	655
Qy	3456	CAATATAGGGTTTTGTTTGGTTGGTTGGTTTGAATAAGCAGTATTTGGGGTCATATTGTT	3515
Db	654	CAATATAGGGTTTTGTTTGGTTGGTTGGTTTGTANAGCAGTATTTGGGGTCATATTGTT	595
Qy	3516	TCCTGTGCTGGAGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATT	3575
Db	594	TCCTGTGCTGGAGCAAAAGTCATTACACTTTGGAGTATTATATTGTTCTTATCCTCAATT	535
Qy	3576	CAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGAT	3635
Db	534	CAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGAT	475
Qy	3636	TGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAA	3695
Db	474	TGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAA	415
Qy	3696	CATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGC	3755
Db	414	CATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGC	355
Qy	3756	AGTCAAATCTATTATTCCTACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGC	3815
Db	354	AGTCAAATCTATTATTCCTACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGC	295
Qy	3816	CATAGGTTACACCATTTTGTTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTT	3875
Db	294	CATAGGTTACACCATTTTGTTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTT	235
Qy	3876	CATATGAAAAAATGCATTTTATAAATTAGAAAGTCATAGATTTCTGAAGGCGTCAACG	3935
Db	234	CATATGAAAAAATGCATTTTATAAATTAGAAAGTCATAGATTTCTGAAGGCGTCAACG	175
Qy	3936	TGCATTTTATTTATGGACTGGTAAGTAACTGTGGTTTACTAGCAGGAATATTTCCAATTT	3995
Db	174	TGCATTTTATTTATGGACTGGTAAGTAACTGTGGTTTACTAGCAGGAATATTTCCAATTT	115
Qy	3996	CTACCTTTACTACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCCAGAAGCCAAAGGCC	4055

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Db      114  |||||CTACCTTTACTACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCC 55
Qy      4056 CTGAGTTGGCAGTGGCCCATAGTGTAAAATAAAAGTTTACAGAAACCTT 4105
Db      54  |||||CTGAGTTGGCAGTGGCCCATAGTGTAAAATAAAAGTTAACAAAACCTT 5

```

RESULT 8

BM719244

LOCUS BM719244 733 bp mRNA linear EST 01-MAR-2002

DEFINITION UI-E-EO1-ajd-b-04-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone  
UI-E-EO1-ajd-b-04-0-UI 5', mRNA sequence.

ACCESSION BM719244

VERSION BM719244.1 GI:19037818

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 733)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).

Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1. .733

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-EO1-ajd-b-04-0-UI"

/tissue\_type="fetal eye"

/dev\_stage="fetal"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-E-EO1"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-E-EO1 is a normalized cDNA library containing the  
following tissue(s): fetal eye. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA



Qy 3762 ATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGG 3821  
 |||  
 Db 600 ATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGG 659

Qy 3822 TTCACACCATTTTGTGTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATG 3881  
 |||  
 Db 660 TTCACACCATTTTGTGTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATG 719

Qy 3882 AAAAAA 3887  
 |||||  
 Db 720 NAAAAA 725

# RESULT 9

BQ018994/c

LOCUS BQ018994 777 bp mRNA linear EST 27-MAR-2002

DEFINITION UI-H-DH1-awv-o-07-0-UI.s1 NCI\_CGAP\_DH1 Homo sapiens cDNA clone  
 IMAGE:5824350 3', mRNA sequence.

ACCESSION BQ018994

VERSION BQ018994.1 GI:19754271

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 777)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Seq primer: M13 FORWARD

POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1..777

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5824350"

/tissue\_type="Metastatic Chondrosarcoma"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI\_CGAP\_DH1"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: EcoR I; Site\_2: Not I;

NCI\_CGAP\_DH1 is a normalized cDNA library containing the  
 following tissue(s): VS-8 Cell line from Metastatic

Chondrosarcoma in Lung. The library was constructed

according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed



with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTGC.

TAG\_LIB=UI-H-DH1

TAG\_TISSUE=lung

TAG\_SEQ=AGATCATTGC"

BASE COUNT            219 a      138 c      166 g      253 t            1 others  
ORIGIN

Query Match                    17.2%;   Score 704.2;   DB 12;   Length 777;  
Best Local Similarity        97.9%;   Pred. No. 1.1e-126;  
Matches   734;   Conservative   0;   Mismatches   14;   Indels        2;   Gaps        2;

```

Qy      1595 TTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAG 1654
          |||||      |||||
Db      750 TATNTGTGAGCAAGAATTTAAAAATGTTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAG 691

Qy      1655 TCCAAAAGTCTGATGACCTCGGTCCCATGAACGGAACAAGCATCCAGTGAAGAACCAC 1714
          |||||
Db      690 TCCAAAAGTCTGATGACCTCGGTCCCATGAACGGAACAAGCATCCAGTGAAGAACCAC 631

Qy      1715 GATCAAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATGAACTGACCACCC 1774
          |||||
Db      630 GATCAAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATGAACTGACCACCC 571

Qy      1775 TTAGAAGCACTCCTCGGTACTCCCATATCCTCTCGGAGAAAAAATCACAAGGCAACTG 1834
          |||||
Db      570 TTAGAAGCACTCCTCGGTACTCCCATATCCTCTCGGAGAAAAAATCACAAGGCAACTG 511

Qy      1835 TGACTCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCCTCACTCCCAACCCAAGAAGA 1894
          |||
Db      510 TGAGTCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCCTCACTCCCAACCCAAGAAGA 451

Qy      1895 AATGCTTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCACCCACAACATCTACGAATCGT 1953
          |||||
Db      450 AATGCTTTTCCAAAACCGCAAGGGTAGACTGGTTTATCCACCCACAACATCTACGAATCGT 391

Qy      1954 ACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGT 2013
          |||||
Db      390 ACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGT 331

Qy      2014 GGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGC 2073
          |||||
Db      330 GGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGC 271

Qy      2074 ATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAA 2133
          |||||
Db      270 ATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAA 211

Qy      2134 TGGGAACTGGTCACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTTAAG 2193
          |||||
Db      210 TGGGAACTGGTCACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTTAAG 151

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Qy      2194 TGA-TTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACTTTTATTTGAAATGT 2252
        ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      150 TGATTTTTTTGTCTTCAGCCAAACACAATATGGGCTCAAGTCACTTTTATTTGAAATGT 91

Qy      2253 CATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACTTATTT 2312
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90  CATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACTTATTT 31

Qy      2313 ACACATAGTTTGAAAAAAAAAAGACAAAAA 2342
        |||||||||||||||||||||||
Db      30  ACACATAGTTTGAAAAAAAAAAGACAAAAA 1

```

RESULT 10

AU139639

LOCUS AU139639 764 bp mRNA linear EST 05-AUG-2002

DEFINITION AU139639 PLACE1 Homo sapiens cDNA clone PLACE1011029 5', mRNA sequence.

ACCESSION AU139639

VERSION AU139639.1 GI:11001160

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 764)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

source

Location/Qualifiers  
 1. .764  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="PLACE1011029"  
 /tissue\_type="placenta"  
 /clone\_lib="PLACE1"  
 /note="Vector: pME18SFL3"

BASE COUNT 252 a 134 c 111 g 263 t 4 others

ORIGIN

Query Match 17.0%; Score 695.8; DB 9; Length 764;  
 Best Local Similarity 97.6%; Pred. No. 4.7e-125;  
 Matches 726; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

Qy	2322	TTGAAAAAAAAAAGACAAAAATAGTATT	CAGGTGAGCAATTAGATTAGTATTTTCCACGT	2381
Db	5	TTTGAAAAAAAAAAGACAAAAATAGTATT	CAGGTGAGCAATTAGATTAGTATTTTCCACGT	64
Qy	2382	CACTATTTATTTTTTTTAAAAACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAA	2441	
Db	65	CACTGTTTATTTTTTTTAAAAACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAA	124	
Qy	2442	AGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGA	2501	
Db	125	AGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGA	184	
Qy	2502	ACTGTATTTTATTTTTTAAATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATG	2561	
Db	185	ACTGTATTTTATTTTTTAAATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATG	244	
Qy	2562	TTAAATTCAAAGTAATGCTTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTT	2621	
Db	245	TTAAATTCAAAGTAATGCTTCAATCAGATAGTTCTTTTTTACAAGTTCAAT-CTGTTTT	303	
Qy	2622	TCATGTAAATTTTGTATGAAAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCAT	2681	
Db	304	TCATGTAAATTTTGTATGAAAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCAT	363	
Qy	2682	TTAACTCTGCCTGAGACTTTCAGTGCACGTGTATATAGAAGTCTAAAACACACCTAAGAGA	2741	
Db	364	TTAACTCTGCCTGAGACTTTCAGTGCACGTGTATATAGAAGTCTACAACACACCTAAGAGA	423	
Qy	2742	AAAAGATCGAATTTTTTCAGATGATTCGGAATTTTCATTTCAGGTATTTGTAATAGTGACA	2801	
Db	424	AAAAGATCGAATTTTTTCAGATGATTCAGAAATTTTCATTTCAGGTATTTGTAATAGTGACA	483	
Qy	2802	TATATATGTATATACATATCACCTCCTATTCTCTTAATTTTTTGTAAAAATGTTAACTGGC	2861	
Db	484	TATATATGTATATACATATCACCTCCTATTCTCTTAATTTTTTCTTAAATGTTAACTGGC	543	
Qy	2862	AGTAAGTCTTTTTTGATCATTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAG	2921	
Db	544	AGTAAGTCTTTTTTGATCATTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGNCAG	603	
Qy	2922	ATGAGTTTATCATGTGTCAGTGAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGAT	2981	
Db	604	ATGAGTTTATCATGTGTCAGTGAAAAATAATTACCCACAAATGCCACCAG--AACTTACGAT	661	
Qy	2982	TCTTCACTTCTTGGGGTTTTTCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCA	3041	
Db	662	TCCTCACTTCTTGGGGTTTTTCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCA	721	
Qy	3042	CATTGTCACCATTTCAAAGGGCCC	3065	
Db	722	CATTGGCACCANTTCAAAGGGGNC	745	

RESULT 11

CD246193

LOCUS

CD246193

782 bp

mRNA

linear

EST 22-MAY-2003



Qy	605	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	129	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	188
Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	724
Db	189	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	248
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	784
Db	249	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	308
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	309	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	368
Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	369	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	428
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	429	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	488
Qy	965	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	489	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	548
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCTTTG	1084
Db	549	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCTTTG	608
Qy	1085	GTAAGTGGCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTTCCTGAA	1144
Db	609	GTAAGTGGCATTGAAATTGTCTCCCTCTGGATCCTGTCTTTATCCTGGCCATTTCCTGAA	668
Qy	1145	GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGG	1182
Db	669	GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGG	706

# RESULT 12

AI694278/c

LOCUS AI694278 739 bp mRNA linear EST 17-DEC-1999

DEFINITION wd45a01.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:2331048 3' similar to gb:S57498 ENDOTHELIN-1 RECEPTOR  
PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI694278

VERSION AI694278.1 GI:4971618

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 739)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),



```

      |||
Db      441 GCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAA 382
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Qy      3730 GAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCATATG 3789
      |||
Db      381 GAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCATATG 322
      |||
Qy      3790 CAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAATTGTC 3849
      |||
Db      321 CAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAATTGTC 262
      |||
Qy      3850 TTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTCAGAAA 3909
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Db      261 TTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTCAGAAA 202
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Qy      3910 GTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAGTGTGG 3969
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Db      201 GTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAGTGTGG 142
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Qy      3970 TTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTAACTTT 4029
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Db      141 TTTACTAGCAGGACTATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTAACTTT 82
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Qy      4030 GTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAAAATAAA 4089
      |||
Db      81 GTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAAAATAAA 22
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Qy      4090 AGTTTACAGAAACCTT 4105
      |||
Db      21 AGTTTACAGAAACCTT 6

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# RESULT 13

BQ575745/c

LOCUS BQ575745 732 bp mRNA linear EST 19-JUN-2002

DEFINITION UI-H-EZ1-bbg-h-22-0-UI.s1 NCI\_CGAP\_Ch2 Homo sapiens cDNA clone  
UI-H-EZ1-bbg-h-22-0-UI 3', mRNA sequence.

ACCESSION BQ575745

VERSION BQ575745.1 GI:21479062

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 732)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of  
Orthopaedics

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES  
source Location/Qualifiers  
1. .732  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-EZ1-bbg-h-22-0-UI"  
/tissue\_type="Chondrosarcoma Grade II"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_Ch2"  
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)  
with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
NCI\_CGAP\_Ch2 is a normalized cDNA library containing the  
following tissue(s): Chondrosarcoma Grade II. The library  
was constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT7T3-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
TGATCACGCT.  
TAG\_LIB=UI-H-EZ1  
TAG\_TISSUE=grade-2-chondrosarcoma  
TAG\_SEQ=ATCTAATATG"  
BASE COUNT 242 a 146 c 110 g 231 t 3 others  
ORIGIN

Query Match 16.9%; Score 692.2; DB 13; Length 732;  
Best Local Similarity 99.1%; Pred. No. 2.4e-124;  
Matches 694; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3406 TACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGG 3465  
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Db 718 TANCAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGG 659  
  
Qy 3466 TTTTGTGGTTGGTTGGTTGGTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTG 3525  
|||||||||||||||||||| ||||||||||||||||||||||||||||||||||||  
Db 658 TTTTGTGGTTGGTTGGTTGNTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTG 599  
  
Qy 3526 GAGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTG 3585  
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Db 598 GAGCAAAAGTCATTACACTNTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTG 539  
  
Qy 3586 ATGAAATTGCCAGGTTGTCTGATATTTCTTTGAGCTTCGCCAGACAGATTGCTGATAAT 3645  
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Db 538 ATGAAATTGCCAGGTTGTCTGATATTTCTTTGAGCTTCGCCAGACAGATTGCTGATAAT 479  
  
Qy 3646 AAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTTC 3705  
|||||||||||||||||||| ||||||||||||||||||||||||||||||||||||  
Db 478 AAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTTC 419



Qy 3706 CAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCT 3765  
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 Db 418 CAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCT 359  
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 Qy 3766 ATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCA 3825  
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 Db 358 ATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCA 299  
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 Qy 3826 CACCATTTTGTTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAA 3885  
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 Db 298 CACCATTTTGTTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAA 239  
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 Qy 3886 AAATGCATTTTATAAATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTAT 3945  
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 Db 238 AAATGCATTTTATAAATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTAT 179  
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 Qy 3946 TTATGGACTGGTAAGTAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTAC 4005  
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 Db 178 TTATGGACTGGTAAGTAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTAC 119  
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 Qy 4006 TACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGC 4065  
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 Db 118 TACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGC 59  
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 Qy 4066 AGTGGCCCATAGTGTAAAATAAAAGTTTACAGAAACCTT 4105  
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 Db 58 AGTGGCCCATAGTGTAAAATAAAAGTTTACAGAAACCTT 19  
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# RESULT 14

AI809396/c

LOCUS AI809396 747 bp mRNA linear EST 19-DEC-1999  
 DEFINITION wf70b01.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
 IMAGE:2360905 3' similar to gb:S57498 ENDOTHELIN-1 RECEPTOR  
 PRECURSOR (HUMAN);, mRNA sequence.  
 ACCESSION AI809396  
 VERSION AI809396.1 GI:5395962  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 747)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Insert Length: 1717 Std Error: 0.00  
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 High quality sequence stop: 466.  
 FEATURES Location/Qualifiers  
 source 1. 747  
 /organism="Homo sapiens"

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/mol_type="mRNA"
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

```

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BASE COUNT      250 a      154 c      118 g      221 t      4 others
ORIGIN

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Query Match          16.8%; Score 687.8; DB 9; Length 747;
Best Local Similarity 98.1%; Pred. No. 1.7e-123;
Matches 725; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

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Qy      3368 ACCTTCTGCATTTCATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATAAGAGGCCA 3427
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Db      742 ACCTTCTGCATTTCAT-AATCTGGTAATCATG-TACCATACNNAATGGGATATAAGAGGCCA 685

Qy      3428 GCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGG-TTGGTTT 3486
          ||||||| ||||||||||||||||||||||||||||||||||||| || ||||| |
Db      684 GCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTGGGTTTGGTNT 625

Qy      3487 GATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTT 3546
          ||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||
Db      624 GATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTT 565

Qy      3547 GAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTG 3606
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Db      564 GAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGGTCTG 505

Qy      3607 ATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTTGT 3666
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Db      504 ATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTTGT 445

Qy      3667 TGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGC 3726
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Db      444 TGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGC 385

Qy      3727 TAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCAT 3786
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Db      384 TAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCAT 325

Qy      3787 ATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAATT 3846
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Db      324 ATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAATT 265

Qy      3847 GTCTTTTTTTTCAAGATGCTTTTGTCTTTTCATATGAAAAAATGCATTTTATAAATTCAG 3906

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Db      264 GTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTCAG 205
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Qy      3907 AAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAACTG 3966
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Db      204 AAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAACTG 145
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Qy      3967 TGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTAAC 4026
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Db      144 TGGTTTACTAGCAGGACTATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTAAC 85
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Qy      4027 TTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAATAAT 4086
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Db      84 TTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAATAAT 25
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Qy      4087 AAAAGTTTACAGAAACCTT 4105
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Db      24 AAAAGTTTACAGAAACCTT 6

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# RESULT 15

BQ006584/c

LOCUS BQ006584 705 bp mRNA linear EST 26-MAR-2002

DEFINITION UI-H-EI1-aza-f-14-0-UI.s1 NCI\_CGAP\_EI1 Homo sapiens cDNA clone  
IMAGE:5846029 3', mRNA sequence.

ACCESSION BQ006584

VERSION BQ006584.1 GI:19731484

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 705)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES Location/Qualifiers

source

1. .705

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5846029"

/tissue\_type="Chondrosarcoma"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI\_CGAP\_EI1"



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Qy      3960  GTAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAAC 4019
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Db      165  GTAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAAC 106

Qy      4020  AAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGT 4079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      105  AAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGT 46

Qy      4080  GTAAAATAAAAGTTTACAGAAACCTT 4105
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Db      45  GTAAAATAAAAGTTTACAGAAACCTT 20

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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:18:36 ; Search time 258.387 Seconds  
 (without alignments)  
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Scoring table: IDENTITY\_NUC  
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Searched: 569978 seqs, 220691566 residues

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Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	4301	100.0	4301	4 US-08-121-446-3	Sequence 3, Appli
2	1691.8	39.3	1873	3 US-08-910-864-13	Sequence 13, Appl
3	1466.8	34.1	1470	4 US-09-016-434-1203	Sequence 1203, Ap
4	1070.4	24.9	1321	4 US-09-175-658B-20	Sequence 20, Appl
5	395.8	9.2	4079	4 US-09-016-434-1257	Sequence 1257, Ap
6	395.8	9.2	4105	4 US-08-121-446-1	Sequence 1, Appli
7	132.2	3.1	1700	5 PCT-US92-02091-1	Sequence 1, Appli
8	114.6	2.7	246240	2 US-08-724-394A-20	Sequence 20, Appl
9	114.6	2.7	246240	2 US-08-724-394A-21	Sequence 21, Appl
10	114.6	2.7	246240	2 US-08-724-394A-22	Sequence 22, Appl
11	108.8	2.5	1584	5 PCT-US92-02091-5	Sequence 5, Appli

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	15	106	2.5	1726	4	US-09-016-434-1215	Sequence 1215, Ap
	16	106	2.5	1726	5	PCT-US92-02091-3	Sequence 3, Appli
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	20	98.6	2.3	1563	1	US-08-910-092-1	Sequence 1, Appli
	21	89.6	2.1	259	4	US-09-016-434-921	Sequence 921, App
	22	88	2.0	1842	4	US-09-170-496D-91	Sequence 91, Appl
	23	88	2.0	1842	4	US-09-170-496D-211	Sequence 211, App
	24	88	2.0	4953	4	US-09-620-312D-240	Sequence 240, App
	25	84.8	2.0	4156	1	US-08-465-687A-1	Sequence 1, Appli
	26	84.8	2.0	4156	3	US-09-030-970-1	Sequence 1, Appli
	27	84.8	2.0	4156	4	US-09-520-210-1	Sequence 1, Appli
	28	84.8	2.0	4156	5	PCT-US94-11843-1	Sequence 1, Appli
	29	80.6	1.9	1443	3	US-08-959-381A-3	Sequence 3, Appli
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	32	80.6	1.9	1626	3	US-08-959-381A-4	Sequence 4, Appli
c	33	63.4	1.5	20674	4	US-09-641-638-651	Sequence 651, App
	34	63.2	1.5	595	1	US-08-784-289-1	Sequence 1, Appli
	35	61.8	1.4	1605	4	US-09-676-970-1	Sequence 1, Appli
	36	61.8	1.4	1605	4	US-09-676-972B-1	Sequence 1, Appli
	37	61.8	1.4	1605	4	US-09-016-434-1231	Sequence 1231, Ap
	38	61.8	1.4	1605	4	US-09-676-941A-1	Sequence 1, Appli
	39	61.8	1.4	1605	4	US-10-013-846-3	Sequence 3, Appli
	40	61.8	1.4	2624	1	US-08-232-144-3	Sequence 3, Appli
	41	61.8	1.4	4571	1	US-08-232-144-5	Sequence 5, Appli
	42	60.8	1.4	511	4	US-09-175-658B-22	Sequence 22, Appl
c	43	60.6	1.4	1864	4	US-09-468-265-4	Sequence 4, Appli
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	45	60.2	1.4	1152	3	US-09-045-186-3	Sequence 3, Appli

#### ALIGNMENTS

#### RESULT 1

US-08-121-446-3

; Sequence 3, Application US/08121446

; Patent No. 6313276

; GENERAL INFORMATION:

; APPLICANT: IMURA, HIROO

; APPLICANT: NAKAO, KAZUWA

; APPLICANT: NAKANISHI, SHIGETADA

; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 238..1566
US-08-121-446-3

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Query Match          100.0%; Score 4301; DB 4; Length 4301;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
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Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

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Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200

Qy 1201 GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 |||  
 Db 1201 GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260

Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAAC'TTTTG 1320  
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 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAAC'TTTTG 1320

Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
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 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380

Qy 1381 AACC'CAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC'TGCTTTAAGTCATGCTTA 1440  
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 Db 1381 AACC'CAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC'TGCTTTAAGTCATGCTTA 1440

Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
 |||  
 Db 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500

Qy 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 1560  
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 Db 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 1560

Qy 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCA'TTTTCTTTATATTGGACCGAAGTCATTAA 1620  
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 Db 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCA'TTTTCTTTATATTGGACCGAAGTCATTAA 1620

Qy 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680  
 |||  
 Db 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680

Qy 1681 TAAAATATTAAGTGTAATTATTTTAACTCACTACAGCTACATATGACATTTTATGAGCTGT 1740  
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 Db 1681 TAAAATATTAAGTGTAATTATTTTAACTCACTACAGCTACATATGACATTTTATGAGCTGT 1740

Qy 1741 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT 1800  
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 Db 1741 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT 1800

Qy 1801 TTTT'TACAGTTAGCACTTCAACATAGCTCTTAACAAC'TCCAGGATATTCACACAACACT 1860  
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 Db 1801 TTTT'TACAGTTAGCACTTCAACATAGCTCTTAACAAC'TCCAGGATATTCACACAACACT 1860

Qy 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT'TA 1920  
 |||  
 Db 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT'TA 1920

Qy 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG 1980  
 |||  
 Db 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG 1980

Qy 1981 AAGCTTAAATTA'CTCAATTTAAAATTTTAAAATCCTTTAAAACAAC'TTTTCAATTAATAT 2040  
 |||  
 Db 1981 AAGCTTAAATTA'CTCAATTTAAAATTTTAAAATCCTTTAAAACAAC'TTTTCAATTAATAT 2040

Qy 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100

Db	2041	 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTGTGTCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	 TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	 CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	2281	 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	2341	 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	 GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	 GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940

Db	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTATATAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3841 CAGCTCAAAGATTATATAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAAAAA 4301  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAAAAA 4301

RESULT 2

US-08-910-864-13

; Sequence 13, Application US/08910864

; Patent No. 6280931

; GENERAL INFORMATION:

; APPLICANT: SAKAMOTO, AIJI

; APPLICANT: HANAOKA, FUMIO

; TITLE OF INVENTION: METHOD FOR SPECIFICALLY AMPLIFYING A cDNA OF AN  
 EXTREMELY

; TITLE OF INVENTION: SMALL QUANTITY

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FISH & RICHARDSON P.C.

; STREET: 4225 EXECUTIVE SQUARE, SUITE 1400

; CITY: LA JOLLA

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:



Qy	538	AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC	597
Db	531	AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC	590
Qy	598	ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC	657
Db	591	ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC	650
Qy	658	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	717
Db	651	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	710
Qy	718	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA	777
Db	711	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	957
Db	891	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAATTTT	1077
Db	1011	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTATTCAATTTT	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAAATGATCCCAATAGATGTGAACTT	1317
Db	1251	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAAATGATCCCAATAGATGTGAACTT	1310
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1370

Qy 1378 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC 1437  
 |||  
 Db 1371 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC 1430

Qy 1438 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1497  
 |||  
 Db 1431 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1490

Qy 1498 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1557  
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 Db 1491 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1550

Qy 1558 TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT 1617  
 |||  
 Db 1551 TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT 1610

Qy 1618 TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACAC 1677  
 |||  
 Db 1611 TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACAC 1670

Qy 1678 TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1737  
 |||  
 Db 1671 TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1730

Qy 1738 TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1797  
 |||  
 Db 1731 TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1790

Qy 1798 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1857  
 |||  
 Db 1791 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1850

Qy 1858 ACTTAGGCTTAAAAATGAGCTCA 1880  
 |||  
 Db 1851 ACTTAGGCTTAAAAATGAGCTCA 1873

# RESULT 3

US-09-016-434-1203

; Sequence 1203, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible



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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HERewith
;      CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;      INFORMATION FOR SEQ ID NO:  1203:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  1470 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g182275
US-09-016-434-1203

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Query Match          34.1%;  Score 1466.8;  DB 4;  Length 1470;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1468;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

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Qy      192  GAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC 251
          |||
Db      1    GAAACTGCGGACGGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC 60

Qy      252  AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGGATCTG 311
          |||
Db      61  AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGGATCTG 120

Qy      312  GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT 371
          |||
Db      121  GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT 180

Qy      372  AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC 431
          |||
Db      181  AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC 240

Qy      432  GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT 491
          |||
Db      241  GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT 300

Qy      492  CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC 551
          |||
Db      301  CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC 360

Qy      552  GGTGTGTCTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAAT 611

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Db	361	 GGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCCACACTTCTGAGAAT	420
Qy	612	TATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT	671
Db	421	 TATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT	480
Qy	672	GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA	731
Db	481	 GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA	540
Qy	732	GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGT	791
Db	541	 GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGT	600
Qy	792	GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC	851
Db	601	 GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC	660
Qy	852	TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGAT	911
Db	661	 TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGAT	720
Qy	912	TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT	971
Db	721	 TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT	780
Qy	972	GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT	1031
Db	781	 GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT	840
Qy	1032	CATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTCTATTTCTGCTTGCC	1091
Db	841	 CATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTCTATTTCTGCTTGCC	900
Qy	1092	ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG	1151
Db	901	 ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG	960
Qy	1152	TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT	1211
Db	961	 TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT	1020
Qy	1212	CTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT	1271
Db	1021	 CTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT	1080
Qy	1272	GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTT	1331
Db	1081	 GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTT	1140
Qy	1332	GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCCTGCATTAAACCAATTGC	1391
Db	1141	 GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCCTGCATTAAACCAATTGC	1200
Qy	1392	TCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTATGCTGCTGGTG	1451

```

Db      1201 TCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTG 1260
Qy      1452 CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC 1511
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC 1320
Qy      1512 TAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1571
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 TAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1380
Qy      1572 GAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAACAAAATGAA 1631
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAACAAAATGAA 1440
Qy      1632 ACATTTGCCAAAACAAAACAAAAAACTATG 1661
        ||||||||||||||||||||||||||||
Db      1441 ACATTTGCCAAAACAAAACAAAAAACTATG 1470

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#### RESULT 4

US-09-175-658B-20

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; Sequence 20, Application US/09175658B
; Patent No. 6372900
; GENERAL INFORMATION:
; APPLICANT: METALLINOS, DANIKA
; APPLICANT: RINE, JASPER
; APPLICANT: BOWLING, ANN
; TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS
; FILE REFERENCE: GOBR-110
; CURRENT APPLICATION NUMBER: US/09/175,658B
; CURRENT FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/062,562
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Horse
US-09-175-658B-20

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Query Match          24.9%; Score 1070.4; DB 4; Length 1321;
Best Local Similarity 88.7%; Pred. No. 6.1e-243;
Matches 1171; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

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Qy      227 CAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTC 286
        |||||||||||||||||||| ||| |||| |||||| |||||| ||||| |||
Db      1   CAGGTAGCAGCATGCAGCCTCTGCCAACCTGTGTGGACGCGTTCTGGTGGCGCTGATCC 60
Qy      287 TTGCCTGCGGCCCTGTTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCA 346
        |||||||| || | || || |||| |||| | |||||| |||||| |||
Db      61 TTGCCTGCGGCGTGGCAGGGGTCCAGGGAGAAGAGAGGAGATTCCCGCCGGCCAGGGCCA 120
Qy      347 CTCCG---CTTTTGCAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCA 403
        ||||| ||| || | || |||||||||||| || |||||| ||||| |||
Db      121 CTCCGCCACTTCTGGGGTCTGAAGAGATAATGACGCCCCGACTAAGACCTCCTGGCCGA 180

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Qy	404	AGGGTTCCAACGCCAGTCTGGCGCGGTCTGTCACCTGCGGAGGTGCCTAAAGGAGACA	463
Db	181	CGGGGTCCAACGCCAGCGTGCCGCGGTCTATCAGCACCTCCGCAAATGCCTAAAGCAGGGA	240
Qy	464	GGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGA	523
Db	241	GGACGGCGGGAGCCCAGCGACGCACCTCCCTCCTCCCCCGTGCGAAAGAACCATCGAGA	300
Qy	524	TCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGA	583
Db	301	TCAAGGAGACTTTCAAGTACATCAACACAGTAGTGTCTGCCTAGTGTTCGTGCTGGGCA	360
Qy	584	TCATCGGGAACTCCACACTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTC	643
Db	361	TCATCGGAACTCCACACTGCTGAGAATCATTTACAAGAACAAAGTGCATGCGGAACGGCC	420
Qy	644	CCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCC	703
Db	421	CTAATATCTTGATCGCCAGCCTGGCTCTCCGAGACCTGCTGCAAATCATCATTGACGTCC	480
Qy	704	CTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGC	763
Db	481	CCATCAATGTCTACAAGCTGCTGGCTGAGGACTGGCCCTTTGGAGTCGAGATGTGTAAGC	540
Qy	764	TGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGA	823
Db	541	TGGTGCCTTTTCATACAGAAGGCCTCCGTGGGCATCACTGTGCTGAGTCTGTGTGCTCTAA	600
Qy	824	GTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAA	883
Db	601	GTATTGACAGATATCGAGCTGTTGCTTCTTGGAGCGAATTAAAGGAATTGGGGTTCCAA	660
Qy	884	AATGGACAGCAGTAGAAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTG	943
Db	661	AATGGACAGCAGTAGAAAATTGTTTTAATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTG	720
Qy	944	AAGCCATAGGTTTTTGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCT	1003
Db	721	AAGCCGTGGGTTTTTGATATGATTACCGCTGACTACAAAGGAAGTTATCTGCGAATCTGCC	780
Qy	1004	TGCTTCATCCCGTTTCTGAGACAGCTTTTATGCAGTTTTTACAAGACAGCAAAAGATTGGT	1063
Db	781	TGCTTCATCCCACTCAGAAAAAGCCTTATGCAGTTTTTACAAGAATGCTAAGGACTGGT	840
Qy	1064	GGCTGTTTCAAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAA	1123
Db	841	GGCTATTTAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACCTTGA	900
Qy	1124	TGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAA	1183
Db	901	TGACCTGTGAAATGTTGAGAAAGAAGAGTGGCATGCAAATTGCTTTAAATGATCACTTAA	960
Qy	1184	AGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCT	1243
Db	961	AGCAGAGAAGGGAAGTGGCGAAAACAGTATTCTGCCTGGTCCTTGTCTTTGCCCTGTGCT	1020
Qy	1244	GGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCA	1303

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      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1021 GGCTTCCTCTTCACCTCAGCAGGATTTTGAAACACACTCTTTATGATCAGAATGATCCCC 1080
Qy      1304 ATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTT 1363
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1081 ATAGATGTGAACTTTTGAGCTTTTGTGGTATTGGACTACATTGGCATCAACATGGCCT 1140
Qy      1364 CACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC 1423
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1141 CCCTGAATTCCTGCATTAATCCAATAGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC 1200
Qy      1424 GCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGG 1483
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1201 GCTTTAAGTCGTGCTTATGCTGCTGGTGCCAATCATTTGAAGAAAAACAGTCCTTGAAG 1260
Qy      1484 AAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCA 1543
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1261 ACAAGCAGTCATGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCA 1320

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RESULT 5

US-09-016-434-1257

; Sequence 1257, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

```

; INFORMATION FOR SEQ ID NO: 1257:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4079 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GENBANK
;   CLONE: g219649
US-09-016-434-1257

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Query Match          9.2%; Score 395.8; DB 4; Length 4079;
Best Local Similarity 65.7%; Pred. No. 1.3e-83;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      685 TGCCCACAGCAGACTAAATTACTTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 744

Qy      565 CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      745 ACTATTTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 804

Qy      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      805 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 864

Qy      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      865 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 924

Qy      741 -----ATTTGGAGCTGAGATGTGTAAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      925 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTCGAGAAGTCCTCG 984

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      985 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC 1044

Qy      850 TCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1045 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCCTTTGGTAACTGCCATTGAAATTGTCTCC 1104

Qy      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTTGATATAATTACG 969
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1105 ATCTGGATCCTGTCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTTCATGGTACCC 1164

Qy      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT 1029
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1165 TTTGAATATAGGGGTGAACAGCATAAACCTGTATGCTCAATGCC-----ACATCAAAA 1218

Qy      1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCACTTTCTATTTCTGCTTG 1089
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      1219 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1278

Qy      1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1146
      || | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 1279 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1338

Qy 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206  
 || | ||| |||| | | ||| || || ||||| || || ||||| || ||

Db 1339 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1398

Qy 1207 ACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGG 1266  
 || || || || || || || || | | ||||| || ||||| || || ||||| || || ||

Db 1399 ACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT 1458

Qy 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT 1326  
 || ||||| || || ||||| || || || ||||| || || ||||| || || ||

Db 1459 ATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1518

Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386  
 | || | |||| || || ||||| || || ||||| || || ||||| || || |||||

Db 1519 TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC 1578

Qy 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1446  
 || ||||| ||||| ||||| || || ||||| || || ||||| || || |||||

Db 1579 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1638

Qy 1447 TGGTG 1451  
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Db 1639 TGCTG 1643

RESULT 6

US-08-121-446-1

; Sequence 1, Application US/08121446  
 ; Patent No. 6313276  
 ; GENERAL INFORMATION:  
 ; APPLICANT: IMURA, HIROO  
 ; APPLICANT: NAKAO, KAZUWA  
 ; APPLICANT: NAKANISHI, SHIGETADA  
 ; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/121,446  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/911,684  
 ; FILING DATE: 10-JUL-1992  
 ; ATTORNEY/AGENT INFORMATION:

```

;      NAME:  CIOTTI, THOMAS E.
;      REGISTRATION NUMBER:  21,013
;      REFERENCE/DOCKET NUMBER:  29900-20324.00
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;      INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  4105 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  485..1768
;      FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  545
US-08-121-446-1

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Query Match          9.2%;  Score 395.8;  DB 4;  Length 4105;
Best Local Similarity 65.7%;  Pred. No. 1.3e-83;
Matches 634;  Conservative 0;  Mismatches 307;  Indels 24;  Gaps 3;

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Qy      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564
        ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      689 TGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Qy      565 CTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACACTTCTGAGAATTATCTACAAGAAC 624
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTACCAGAAC 808

Qy      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
        || | | | | | | | | | | | | | | | | | | | | | |
Db      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868

Qy      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740
        | | | | | | | | | | | | | | | | | | | | | |
Db      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928

Qy      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
        | | | | | | | | | | | | | | | | | | | | | |
Db      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAGTCCTCG 988

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
        ||||| ||||| | | | | | | | | | | | | | | | |
Db      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048

Qy      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909
        || | | | | | | | | | | | | | | | | | | | | |
Db      1049 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTTCCTTTGGTAAGTGCATTGAAATTGTCTCC 1108

Qy      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969
        || | | | | | | | | | | | | | | | | | | | |
Db      1109 ATCTGGATCCTGTCCTTTATCCTGGCCATTTCCTGAAGCGATTGGCTTCGTATGGTACCC 1168

```



Qy 970 ATGGA CTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT CAGAAGACAGCT 1029  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222

Qy 1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTT CAGTTTCTATTTCTGCTTG 1089  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282

Qy 1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAG 1146  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342

Qy 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402

Qy 1207 ACCGTCCTTTTGCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG 1266  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1403 ACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462

Qy 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT 1326  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1463 ATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522

Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1523 TTA CTGCTCATGGATTACATCGGTATTA ACTTGGCAACCATGAATTCATGTATAAACCCC 1582

Qy 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC TGTCTTAAGTCATGCTTATGCTGC 1446  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642

Qy 1447 TGGTG 1451  
 | | | |  
 Db 1643 TGCTG 1647

# RESULT 7

PCT-US92-02091-1

; Sequence 1, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

; STATE: CA

; COUNTRY: USA

; ZIP: 94501

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US92/02091
;   FILING DATE:  19920313
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/426,150
;   FILING DATE:  24-OCT-1989
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/533,659
;   FILING DATE:  05-JUN-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Ching, Edwin P.
;   REGISTRATION NUMBER:  34090
;   REFERENCE/DOCKET NUMBER:  A-0092C
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-266-7476
;   TELEFAX:  415-266-7400
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1700 base pairs
;   TYPE:  NUCLEIC ACID
;   STRANDEDNESS:  double
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   HYPOTHETICAL:  NO
;   ORIGINAL SOURCE:
;   ORGANISM:  Mus musculus
;   CELL LINE:  Swiss 3T3
;   IMMEDIATE SOURCE:
;   LIBRARY:  Lambda GT10
;   FEATURE:
;   NAME/KEY:  CDS
;   LOCATION:  378..1532
PCT-US92-02091-1

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Query Match          3.1%;  Score 132.2;  DB 5;  Length 1700;
Best Local Similarity 56.9%;  Pred. No. 1.4e-21;
Matches 242;  Conservative 0;  Mismatches 183;  Indels 0;  Gaps 0;

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Qy      535 TTCAAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAC 594
        ||||  ||  |||  |  |  |||  |  ||||  |  |||  |  ||  |||  |||
Db      495 TTCATCTATGTCATCCCTGCAGTTTATGGGCTTATCATCGTGATAGGTCTTATTGGCAAC 554

Qy      595 TCCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTG 654
        |||  ||  |  |  ||  |||  ||  |  ||||  |||||  ||||  ||  ||  |||
Db      555 ATCACGCTCATCAAGATCTTCTGCACGGTCAAGTCCATGCGAAACGTGCCAAACCTGTTC 614

Qy      655 ATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTC 714
        |||  |  |||  ||||  |||||  |||||  |||||  |||  |  ||||  |||  |
Db      615 ATCTCTAGCCTGGCTTTGGGAGACCTGCTGCTGCTGGTGACATGCGCCCCCTGTGGATGCC 674

Qy      715 TACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTC 774
        ||||  |||||  ||  ||||  |||||  |||||  ||  ||  |||  |  ||  |||
Db      675 AGCAAGTACCTGGCTGACAGGTGGCTATTTGGCAGAATTGGCTGCAAACCTGATCCCCTTT 734

```

Qy 775 ATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGA 834  
 ||||| | || ||||| | |||| | | || ||||| |||||  
 Db 735 ATACAACTTACTTCAGTGGGGGTGTCTGTCTTCACACTTACGGCACTGTCTGAGCTGACAGG 794  
 Qy 835 TATCGAGCTGTTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCA 894  
 || ||| ||| | ||| | | | | | | | |  
 Db 795 TACAAAGCCATTGTACGGCCAATGGATATCCAGGCATCCCATGCCCTGATGAAGATCTGT 854  
 Qy 895 GTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGT 954  
 | || | ||||| ||| | ||||| ||| | |||| | ||| |  
 Db 855 CTCAAAGCTGCTTTGATCTGGATTGTCTCTATGTTGTTGGCCATCCCAGAGGCTGTGTTT 914  
 Qy 955 TTTGA 959  
 | |||  
 Db 915 TCTGA 919

RESULT 8

US-08-724-394A-20

; Sequence 20, Application US/08724394A

; Patent No. 5872237

; GENERAL INFORMATION:

; APPLICANT: Feder, John N.

; APPLICANT: Kronmal, Gregory S.

; APPLICANT: Lauer, Peter M.

; APPLICANT: Ruddy, David A.

; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

; TITLE OF INVENTION: Sequences and Antibodies Thereto

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,394A

; FILING DATE: 01-OCT-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitts, Renee A.

; REGISTRATION NUMBER: 35,136

; REFERENCE/DOCKET NUMBER: 017957-000100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

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;      LENGTH: 246240 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: not relevant
;      TOPOLOGY: not relevant
;      MOLECULE TYPE: cDNA
;      FEATURE:
;      NAME/KEY: misc_feature
;      LOCATION: 1..246240
;      OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
```

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Query Match          2.7%; Score 114.6; DB 2; Length 246240;
Best Local Similarity 82.0%; Pred. No. 1.8e-16;
Matches 132; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
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```
Qy      5 CATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
      ||| || |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      180691 CATCCCTACGGGGAAGTCCAGCCAGTTTGAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750

Qy      65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810

Qy      125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851
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# RESULT 9

US-08-724-394A-21

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; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

```

```

Query Match          2.7%; Score 114.6; DB 2; Length 246240;
Best Local Similarity 82.0%; Pred. No. 1.8e-16;
Matches 132; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

```

```

Qy          5 CATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
   ||| || |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 180691 CATCCCTACGGGGAACCTCCAGCCAGTTTGAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750

Qy          65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810

Qy          125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851

```

# RESULT 10

US-08-724-394A-22

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; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto

```

```

; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

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Query Match          2.7%; Score 114.6; DB 2; Length 246240;
Best Local Similarity 82.0%; Pred. No. 1.8e-16;
Matches 132; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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```

Qy          5 CATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
             ||| ||  |||| |||| |||| |||| ||| ||| |||| |||| |||| ||||
Db 180691 CATCCCTACGGGAACTCCAGCCAGTTTGAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750

Qy          65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
             |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810

Qy          125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
             |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851

```

RESULT 11

PCT-US92-02091-5  
; Sequence 5, Application PC/TUS9202091  
; GENERAL INFORMATION:  
; APPLICANT: Battey Jr., James F.  
; APPLICANT: Corjay, Martha H.  
; APPLICANT: Feldman, Richard I.  
; APPLICANT: Harkins, Richard N.  
; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Edwin P. Ching  
; STREET: 1501 Harbor Bay Parkway  
; CITY: Alameda  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94501  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/02091  
; FILING DATE: 19920313  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/426,150  
; FILING DATE: 24-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/533,659  
; FILING DATE: 05-JUN-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34090  
; REFERENCE/DOCKET NUMBER: A-0092C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-266-7476  
; TELEFAX: 415-266-7400  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1584 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Rattus rattus  
; TISSUE TYPE: Esophagus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 132..1304  
PCT-US92-02091-5

Query Match 2.5%; Score 108.8; DB 5; Length 1584;  
Best Local Similarity 54.8%; Pred. No. 4.3e-16;  
Matches 215; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy	572	TCGTGCTGGGGATCATCGGGAACCCACACTTCTGAGAATTATCTACAAGAACAAGTGCA	631
Db	292	TCTCGGTGGGCTTGCTGGGCAACATCATGCTGGTGAAGATATTCCTCACCAACAGCACCA	351
Qy	632	TGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCG	691
Db	352	TGCGGAGTGTCCCAACATCTTCATCTCTAACCTGGCTGCGGGAGACCTGCTGCTGCTGC	411
Qy	692	TCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTG	751
Db	412	TGACCTGCGTCCAGTGGATGCCTCCCGATACTTCTTTGATGAATGGGTGTTCCGCAAGC	471
Qy	752	AGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTC	811
Db	472	TGGGCTGCAAACATCATCCAGCCATCCAGCTCACCTCGGTGGGGGTTTCCGTGTTCACTC	531
Qy	812	TATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAA	871
Db	532	TCACGGCCCTCAGCGCTGACAGGTACAGAGCTATCGTGAACCCCATGGACATGCAGACGT	591
Qy	872	TTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTTC	931
Db	592	CTGGTGTGGTGTCTGTGGACCAGTTTGAAGGCCGTGGGCATCTGGGTGGTCTCTGTGCTGT	651
Qy	932	TGGCTGTCCCTGAAGCCATAGGTTTTGATATA	963
Db	652	TGGCTGTCCCTGAGGCTGTGTTTTTCGGAAGTA	683

# RESULT 12

US-09-175-658B-25/c

; Sequence 25, Application US/09175658B

; Patent No. 6372900

; GENERAL INFORMATION:

; APPLICANT: METALLINOS, DANIKA

; APPLICANT: RINE, JASPER

; APPLICANT: BOWLING, ANN

; TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS

; FILE REFERENCE: GOBR-110

; CURRENT APPLICATION NUMBER: US/09/175,658B

; CURRENT FILING DATE: 1998-10-20

; PRIOR APPLICATION NUMBER: 60/062,562

; PRIOR FILING DATE: 1997-10-21

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 801

; TYPE: DNA

; ORGANISM: Horse

; FEATURE:

; OTHER INFORMATION: Uncertain of the nucleotide sequence at positions

; OTHER INFORMATION: 30, 54, 286, 436, 445, 542, 614, 617, 624, 641,

; OTHER INFORMATION: 731, 746, 753, 770, 775 and 793.

US-09-175-658B-25

Query Match

2.5%; Score 107.2; DB 4; Length 801;



Best Local Similarity 86.8%; Pred. No. 7.6e-16;  
Matches 118; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      1408 AAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAA 1467
        ||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      223 AAACGAGTTATTTGTTTTGTACAGTCGTGCTTATGCTGCTGGTGCCAATCATTTGAAGAA 164

Qy      1468 AAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATAT 1527
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      163 AAACAGTCCTTGAAGACAAGCAGTCATGCTTAAAGTTCAAAGCTAATGATCACGGATAT 104

Qy      1528 GACAACTTCCGTTCCA 1543
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      103 GACAACTTCCGTTCCA 88
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RESULT 13

US-09-120-772-1

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; Sequence 1, Application US/09120772
; Patent No. 6143521
; GENERAL INFORMATION:
;   APPLICANT: LANE, PAMELA
;   APPLICANT: TSUI, PING
;   APPLICANT: ELSHOUBAGY, NABIL
;   TITLE OF INVENTION: HUMAN BOMBESIN RECEPTOR SUBTYPE
;   TITLE OF INVENTION: 3
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Ratner & Prestia
;     STREET: P.O. Box 980
;     CITY: Valley Forge
;     STATE: PA
;     COUNTRY: USA
;     ZIP: 19482
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/120,772
;     FILING DATE: 22-JUL-1998
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Prestia, Paul F
;     REGISTRATION NUMBER: 23,031
;     REFERENCE/DOCKET NUMBER: GP-70505
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 610-407-0700
;     TELEFAX: 610-407-0700
;     TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1205 base pairs
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; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-120-772-1

Query Match 2.5%; Score 106.6; DB 3; Length 1205;  
Best Local Similarity 48.5%; Pred. No. 1.3e-15;  
Matches 425; Conservative 0; Mismatches 434; Indels 18; Gaps 4;

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Db      181 TGGGCATCCTTGGAAATGCTATTCTCATCAAAGTCTTTTCAAGACCAAATCCATGCAA 240

Qy      638 ACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTG 697
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Db      241 CAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTT 300

Qy      698 ACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGT 757
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Db      301 GTGTGCCAGTGGATGCAACTCACTACCTTGCAAGGATGGCTGTTCCGAAGAATTGGTT 360

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Db      421 TTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAGCCCTCCAATG 480

Qy      878 TTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTG 937
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Db      481 CCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTGTCTATGATATTTGCTC 540

Qy      938 TCCCTGAAGCCATAGGTTTTGATATA-----ATTACGATGGACTACAAAGGAAGTTATCT 992
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Db      541 TACCTGAGGCTATATTTTCAAATGTATACACTTTTCGAGATCCCAATAAAAATATGACAT 600

Qy      993 GCGAATCTGCTTGCT-TCATCCCGTTTCAAGACAGCTTTTCATGCAGTTTACAAGACAG 1051
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Db      721 TTGCTAGGACCCTTTACAAAAGCACCTGAACATACCTACTGAGGAACAAAGCCATGCCC 780

Qy      1172 ATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCT 1231
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Qy      1232 TTGCCCTCTGCTGGCTTCCCTTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATC 1291
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Qy 1292 AGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATATTGGTA 1351  
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 Db 892 CTTCTCAAACCTATGTA--GACCCCTCTGCCATGCATTTTCATTTTCACCATTTTCTCTC 948  
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 Qy 1412 GATTCAAAAAGCTTTTAAGTCATGCTTATGCTGCTG 1448  
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 Db 1009 GCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTG 1045

RESULT 14

US-09-016-434-1275

; Sequence 1275, Application US/09016434  
 ; Patent No. 6500938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/016,434  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0002 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1275:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1413 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear

; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g291876  
US-09-016-434-1275

Query Match 2.5%; Score 106.6; DB 4; Length 1413;  
Best Local Similarity 48.5%; Pred. No. 1.4e-15;  
Matches 425; Conservative 0; Mismatches 434; Indels 18; Gaps 4;

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      ||||| ||| | ||| | | | | | | | | | | | | | | | | | |
Db      328 TGGGCATCCTTGGAATGCTATTCTCATCAAAGTCTTTTCAAGACCAAATCCATGCAA 387

Qy      638 ACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTG 697
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      388 CAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTT 447

Qy      698 ACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGT 757
      | | | | | | | | | | | | | | | | | | | | | |
Db      448 GTGTGCCAGTGGATGCAACTCACTACCTTGCAAGGATGGCTGTTTCGAAGAATTGGTT 507

Qy      758 GTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTG 817
      ||||| || | | | | | | | | | | | | | | | | | |
Db      508 GTAAGGTGCTCTCTTTTCATCCGGCTCACTTCTGTTGGTGTGTGAGTGTTACATTAAACA 567

Qy      818 CTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGG 877
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Db      568 TTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAGCCCTCCAATG 627

Qy      878 TTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTG 937
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Db      628 CCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTGTCTATGATATTTGCTC 687

Qy      938 TCCCTGAAGCCATAGGTTTTGATATA-----ATTACGATGGACTACAAAGGAAGTTATCT 992
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Db      688 TACCTGAGGCTATATTTTCAAATGTATACACTTTTCGAGATCCCAATAAAAATATGACAT 747

Qy      993 GCGAATCTGCTTGCT-TCATCCCGTTTCAAGACAGCTTTTCATGCAGTTTTACAAGACAG 1051
      ||||| | | | | | | | | | | | | | | | | |
Db      748 TTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAAGAAATACATTCTCTGC 807

Qy      1052 CAAAAGATTGGTGGCTGTTTCACTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTT 1111
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Db      808 TGTGCTTCTTAGTGTTCTACATTATTCCACTCTCTATTATCTCTGTCTACTATTCCTTGA 867

Qy      1112 TTTATACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAA 1171
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Db      868 TTGCTAGGACCCTTTACAAAAGCACCTGAACATACCTACTGAGGAACAAAGCCATGCCC 927

Qy      1172 ATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCT 1231
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Qy      1232 TTGCCCTCTGCTGGCTTCCCTTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATC 1291
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Qy 1292 AGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATATTGGTA 1351  
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 Db 1039 CTTCTCAAACCTATGTA---GACCCCTCTGCCATGCATTTTCAATTTTACCATTTTCTCTC 1095  
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 Db 1096 GGGTTTTGGCTTTTCAGCAATTCTTGCCTAAACCCCTTTGCTCTCTACTGGCTGAGCAAAA 1155  
 Qy 1412 GATTCAAAAAGCTTTTAAGTCATGCTTATGCTGCTG 1448  
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 Db 1156 GCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTG 1192

RESULT 15

US-09-016-434-1215

; Sequence 1215, Application US/09016434  
 ; Patent No. 6500938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/016,434  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0002 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1215:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1726 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:

; LIBRARY: GENBANK  
; CLONE: g183649  
US-09-016-434-1215

Query Match 2.5%; Score 106; DB 4; Length 1726;  
Best Local Similarity 52.0%; Pred. No. 2.1e-15;  
Matches 238; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

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Qy      596 CCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGA 655
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Qy      656 TCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCT 715
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Db      694 GCAGGTACCTGGCTGACAGATGGCTATTTGGCAGGATTGGCTGCAAACCTGATCCCCTTTA 753

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Db      814 ACAAAGCCATTGTCCGGCCAATGGATATCCAGGCCTCCCATGCCCTGATGAAGATCTGCC 873

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Job time : 264.387 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 10:54:32 ; Search time 1259.7 Seconds  
(without alignments)  
11347.756 Million cell updates/sec

Title: US-09-931-157-2  
Perfect score: 4301  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

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	2	4284.4	99.6	4286	13	US-10-007-926A-177	Sequence 177, App
	3	4284.4	99.6	4286	13	US-09-921-406C-13	Sequence 13, Appl
	4	4284.4	99.6	4286	13	US-10-210-120-15	Sequence 15, Appl
	5	4284.4	99.6	4286	15	US-10-225-567A-113	Sequence 113, App
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	7	1322.6	30.8	1329	13	US-09-826-509-496	Sequence 496, App
	8	763.2	17.7	800	9	US-09-778-927A-27	Sequence 27, Appl
c	9	440.6	10.2	592	9	US-09-962-436-531	Sequence 531, App
c	10	440.6	10.2	592	10	US-09-880-107-2060	Sequence 2060, Ap
c	11	440.6	10.2	592	10	US-09-954-531-917	Sequence 917, App
	12	403.4	9.4	405	11	US-09-918-995-7311	Sequence 7311, Ap
	13	395.8	9.2	4105	9	US-09-931-157-1	Sequence 1, Appli
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	15	395.8	9.2	4105	13	US-10-101-510-370	Sequence 370, App
	16	395.8	9.2	4105	15	US-10-225-567A-115	Sequence 115, App
	17	392.6	9.1	1284	13	US-09-826-509-494	Sequence 494, App
	18	311	7.2	390	13	US-10-007-926A-176	Sequence 176, App
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c	20	302	7.0	363	10	US-09-954-456-209	Sequence 209, App
c	21	302	7.0	363	10	US-09-954-456-467	Sequence 467, App
c	22	302	7.0	363	10	US-09-954-456-925	Sequence 925, App
c	23	302	7.0	363	10	US-09-954-456-1550	Sequence 1550, Ap
c	24	302	7.0	363	10	US-09-880-107-2076	Sequence 2076, Ap
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c	26	275	6.4	307	13	US-09-921-406C-12	Sequence 12, Appl
	27	148.8	3.5	1889	10	US-09-867-701-10875	Sequence 10875, A
	28	131.6	3.1	1330	11	US-09-374-046A-151	Sequence 151, App
c	29	128.4	3.0	503	13	US-10-264-283-84	Sequence 84, Appl
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	31	128.4	3.0	888	13	US-10-264-283-93	Sequence 93, Appl
	32	128.2	3.0	668	15	US-10-198-846-13575	Sequence 13575, A
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	36	122.2	2.8	1291	13	US-10-027-632-124978	Sequence 124978,
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	38	118.6	2.8	489	11	US-09-918-995-136	Sequence 136, App
c	39	114.6	2.7	235033	15	US-10-301-844-1	Sequence 1, Appli
c	40	114.6	2.7	237326	15	US-10-301-844-2	Sequence 2, Appli
	41	112	2.6	2595	9	US-09-160-116-11	Sequence 11, Appl
c	42	111.6	2.6	860	15	US-10-198-846-7034	Sequence 7034, Ap
c	43	111	2.6	399	15	US-10-102-806-400	Sequence 400, App
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c	45	109.8	2.6	347	13	US-09-814-353-10877	Sequence 10877, A

#### ALIGNMENTS

#### RESULT 1

US-09-931-157-2

; Sequence 2, Application US/09931157

; Patent No. US20020082414A1

; GENERAL INFORMATION:

; APPLICANT: Imura, Hiroo



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; APPLICANT: Nakao, Kazuwa
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4301
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (238)...(1566)
US-09-931-157-2

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Query Match 100.0%; Score 4301; DB 9; Length 4301;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTTATAATCAGAAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTTATAATCAGAAATGATCCCAATAGATGTGAACTTTTG	1320

Qy	1321	AGCTTTTCTGTTGGTATTGGACTATATTGGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	AGCTTTTCTGTTGGTATTGGACTATATTGGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACCTGTATTTTCATTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACCTGTATTTTCATTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160

Qy	2161	TTTTGAAAAATCATTACACTTTTCACTAGAAAGCCCAAAACCTCAGCATTTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAAATCATTACACTTTTCACTAGAAAGCCCAAAACCTCAGCATTTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTGCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTGCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATT CAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATT CAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAAATAGAAATGTTTGAAAGGCTATCCCAAAAGACTTTTTTTGAATCTGTCATTCA	2400
Db	2341	CAAAGAGAAAATAGAAATGTTTGAAAGGCTATCCCAAAAGACTTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTAATTATTTTTGTAAATAGCCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTTGTAATTATTTTTGTAAATAGCCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTTCTTTTCATCTAGAGGCAAAACTGCTTTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTTCTTTTCATCTAGAGGCAAAACTGCTTTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTTCTAAGCAAAGTGCCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTTCTAAGCAAAGTGCCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060

Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Qy	3541	TCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900

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Db      3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900
Qy      3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
        |||
Db      3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
Qy      3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020
        |||
Db      3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020
Qy      4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
        |||
Db      4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
Qy      4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140
        |||
Db      4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140
Qy      4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200
        |||
Db      4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200
Qy      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
        |||
Db      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
Qy      4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301
        |||
Db      4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301

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## RESULT 2

US-10-007-926A-177

; Sequence 177, Application US/10007926A

; Publication No. US20030143539A1

; GENERAL INFORMATION:

; APPLICANT: BERTUCCI, FRANCOIS

; APPLICANT: HOULGATTE, REMI

; APPLICANT: BIRNBAUM, DANIEL

; APPLICANT: NGUYEN, CATHERINE

; APPLICANT: VIENS, PATRICE

; APPLICANT: FERT, VINCENT

; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

; FILE REFERENCE: 1546-R-00

; CURRENT APPLICATION NUMBER: US/10/007,926A

; CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: 60/254,090

; PRIOR FILING DATE: 2000-12-08

; NUMBER OF SEQ ID NOS: 468

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 177

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: endothelin receptor type b (EDNRB) gene.

US-10-007-926A-177

Query Match 99.6%; Score 4284.4; DB 13; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Db	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCGCTGG	120
Db	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCGCTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCCACA	600
Db	541	TACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780

Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGCAATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGCAATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAGATTCAAAAAGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAGATTCAAAAAGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620



Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCTAGTAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCTAGTAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520

Db	2461	 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360

Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360

Qy 3361 ACAAACTTGTTCTTTAATTTATCCCAATCACTTTTTAGAGGCCTGTTATCATAGAAGT 3420  
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Db 3361 ACAAACTTGTTCTTTAATTTATCCCAATCACTTTTTAGAGGCCTGTTATCATAGAAGT 3420

Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTACAGTTTATTAA 3480  
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Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTACAGTTTATTAA 3480

Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540  
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Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540

Qy 3541 TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
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Db 3541 TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600

Qy 3601 TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
 |||

Db 3601 TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660

Qy 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 |||

Db 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
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Db 3721 TTCTTTACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAATCATGGATGTTA 3840  
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Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAATCATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 |||

Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
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Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
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Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 |||

Db 4021 AAAAAATTATATATCTGGGAGGATTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140  
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Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
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Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200

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Qy      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286
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Db      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

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RESULT 3

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US-09-921-406C-13
; Sequence 13, Application US/09921406C
; Publication No. US20030152923A1
; GENERAL INFORMATION:
; APPLICANT: Yakhini, Zohar
; APPLICANT: Ben-Dor, Amir
; APPLICANT: Sampas, Nick
; APPLICANT: Dougherty, Edward
; APPLICANT: Trent, Jeff
; APPLICANT: Meltzer, Paul
; APPLICANT: Chen, Yidong
; APPLICANT: Weeraratna, Ashani
; APPLICANT: Jiang, Yuan
; APPLICANT: Bittner, Michael
; TITLE OF INVENTION: Classifying Cancers
; FILE REFERENCE: 10010313-1
; CURRENT APPLICATION NUMBER: US/09/921,406C
; CURRENT FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-921-406C-13

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Query Match          99.6%; Score 4284.4; DB 13; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
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Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

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Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT	1080
Db	1021	AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	1140

Db	1081		TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141		AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141		AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201		GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201		GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261		AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261		AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321		AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321		AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381		AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Db	1381		AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Qy	1441		TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441		TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501		AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501		AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561		TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561		TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621		AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621		AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681		TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681		TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741		TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741		TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801		TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801		TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Qy	1861		TAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Db	1861		TAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Qy	1921		AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACGTGTAACAGAACTTTTAAATG	1980

Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAAACAACCTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAAACAACCTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTGTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTGTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820

Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGGAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCTGTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCTGTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Qy	3541	TCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660



Qy 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
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 Db 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
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 Db 3721 TTCTTTACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
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 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
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 Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 |||  
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 |||  
 Db 3961 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 |||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTTC 4140  
 |||  
 Db 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 |||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

#### RESULT 4

US-10-210-120-15

; Sequence 15, Application US/10210120

; Publication No. US20030175736A1

; GENERAL INFORMATION:

; APPLICANT: Chinnaiyan, Arul M.

; APPLICANT: Rubin, Mark A.

; APPLICANT: Sreekumar, Arun

; TITLE OF INVENTION: Expression Profile of Prostate Cancer

; FILE REFERENCE: UM-07221

; CURRENT APPLICATION NUMBER: US/10/210,120

; CURRENT FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: US 60/309,581  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: US 60/334,468  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 15  
; LENGTH: 4286  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-210-120-15

Query Match 99.6%; Score 4284.4; DB 13; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAC TGGTACTTGGAGTCTGGACATCTGA 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAC TGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCC TAAAGGAGACAGGACGGCAGGATCTCCG 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCC TAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy    481 CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTCAA 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTCAA 540

Qy    541 TACATCAACACGGTTGTGTCTTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAAC TCCACA 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TACATCAACACGGTTGTGTCTTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAAC TCCACA 600

Qy    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
```

Db	601	 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAA	900
Db	841	 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTC	1260
Db	1201	 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAAATTCCTGCATT	1380
Db	1321	 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Db	1381	 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCAATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGCTTA	1500

Db	1441	TGCTGCTGGTGCCAGTCACTTTGAAGAAAAACAGTCCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCACTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCACTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAGTGTAATTATTTTAACTCACTACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAGTGTAATTATTTTAACTCACTACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTAAGTCAATTTTAAATTTTAAATCCTTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTAAGTCAATTTTAAATTTTAAATCCTTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTTCGGACACTGGAAACATTTTAAATGATCAGGAGGGAGTAACAGAAAAGCAAGGCTGT	2160
Db	2101	TTTTTCGGACACTGGAAACATTTTAAATGATCAGGAGGGAGTAACAGAAAAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340

Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTGAATCTGTCATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAAAGTCTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAAAGTCTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180

Qy	3181	ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080

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Db      4021  |||||
AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy      4081  TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140
|||||

Db      4081  TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140
|||||

Qy      4141  ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
|||||

Db      4141  ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
|||||

Qy      4201  CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
|||||

Db      4201  CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
|||||

Qy      4261  AAAATGCCACATTTCTGGTCTCTGGG 4286
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Db      4261  AAAATGCCACATTTCTGGTCTCTGGG 4286
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# RESULT 5

US-10-225-567A-113

; Sequence 113, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 113

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-113

Query Match 99.6%; Score 4284.4; DB 15; Length 4286;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1  GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
|||||

Db      1  GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
|||||

Qy      61  AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
|||||

Db      61  AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
|||||

Qy      121  AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180

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Db	121	 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCA	1020



Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAGAAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAGAAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860

Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAACCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAGAACCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	CATACCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCACTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCACTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700

Qy	2701	GCTATAGTTAAAAATACTATTTTTTCAAATCATA CAGATTAGTACATTTAAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAAATACTATTTTTTCAAATCATA CAGATTAGTACATTTAAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAAATTTTTATATCTTCTAAGCAAAGTGCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAAATTTTTATATCTTCTAAGCAAAGTGCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAAATGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAAATGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTTGTTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTTGTTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCTTCTCCATGTGAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600

Db	3541	 TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	4261	 AAAATGCCACATTTCTGGTCTCTGGG	4286

RESULT 6

US-10-020-141-5/c

; Sequence 5, Application US/10020141

; Publication No. US20030092013A1

; GENERAL INFORMATION:

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; APPLICANT: McCarthy, Jeanette
; APPLICANT: Ableson, Allen
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-002
; CURRENT APPLICATION NUMBER: US/10/020,141
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/313,097
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/327,485
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 183337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-020-141-5

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Query Match          66.1%; Score 2841.8; DB 15; Length 183337;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2854; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72830 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 72771

Qy      1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72770 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 72711

Qy      1550 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACC 1609
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72710 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACC 72651

Qy      1610 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAAACAAAAAATACTATGTATTTGCA 1669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72650 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAAACAAAAAATACTATGTATTTGCA 72591

Qy      1670 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATT 1729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72590 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATT 72531

Qy      1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA 1789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72530 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA 72471

Qy      1790 AAGCACTTAATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 1849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72470 AAGCACTTAATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 72411

Qy      1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAG 1909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72410 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAG 72351

Qy      1910 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGA 1969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72350 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGA 72291

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Qy	1970	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTTT	2029
Db	72290	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTTT	72231
Qy	2030	TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	2089
Db	72230	TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	72171
Qy	2090	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG	2149
Db	72170	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG	72111
Qy	2150	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTG	2209
Db	72110	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTG	72051
Qy	2210	CAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	2269
Db	72050	CAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	71991
Qy	2270	TGAATTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTTAAG	2329
Db	71990	TGAATTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTTAAG	71931
Qy	2330	ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA	2389
Db	71930	ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA	71871
Qy	2390	TCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	2449
Db	71870	TCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	71811
Qy	2450	ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	2509
Db	71810	ATCTTCTTCTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	71751
Qy	2510	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	2569
Db	71750	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	71691
Qy	2570	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCAC	2629
Db	71690	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCAC	71631
Qy	2630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC	2689
Db	71630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC	71571
Qy	2690	ATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTA	2749
Db	71570	ATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTA	71511
Qy	2750	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	2809
Db	71510	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	71451

Qy	2810	AAGTTTGGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAACCTGCTTTTTTGAGACCGT	2869
Db	71450	AAGTTTGGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAACCTGCTTTTTTGAGACCGT	71391
Qy	2870	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCCT	2929
Db	71390	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCCT	71331
Qy	2930	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	2989
Db	71330	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	71271
Qy	2990	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTT	3049
Db	71270	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTT	71211
Qy	3050	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCTTGATTTTGTTCAGCAAAACACAGTG	3109
Db	71210	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCTTGATTTTGTTCAGCAAAACACAGTG	71151
Qy	3110	CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	3169
Db	71150	CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	71091
Qy	3170	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGAAATA	3229
Db	71090	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGAAATA	71031
Qy	3230	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAA	3289
Db	71030	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAA	70971
Qy	3290	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTT	3349
Db	70970	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTT	70911
Qy	3350	ATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	3409
Db	70910	ATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	70851
Qy	3410	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	3469
Db	70850	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	70791
Qy	3470	CAGTTTATTAATATATTTTAAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	3529
Db	70790	CAGTTTATTAATATATTTTAAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	70731
Qy	3530	GAATTTTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	3589
Db	70730	GAATTTTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	70671
Qy	3590	TTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCA	3649
Db	70670	TTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCA	70611
Qy	3650	TTCAGTGGCTTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA	3709

Db	70610	 TTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA	70552
Qy	3710	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	3769
Db	70551	 ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	70492
Qy	3770	TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	3829
Db	70491	 TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	70432
Qy	3830	CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	3889
Db	70431	 CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	70372
Qy	3890	CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	3949
Db	70371	 CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	70312
Qy	3950	AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	4009
Db	70311	 AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	70252
Qy	4010	TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	4069
Db	70251	 TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	70192
Qy	4070	GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTA	4129
Db	70191	 GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTA	70132
Qy	4130	CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA	4189
Db	70131	 CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA	70072
Qy	4190	TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA	4249
Db	70071	 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA	70012
Qy	4250	GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	4286
Db	70011	 GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	69975

RESULT 7

US-09-826-509-496

; Sequence 496, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509





Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	601	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	660
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	957
Db	661	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	720
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	721	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	780
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	781	CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	840
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	841	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	900
Qy	1138	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	901	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	960
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	961	GTGAAGAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1020
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
Db	1021	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1080
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCCTGC	1377
Db	1081	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCCTGC	1140
Qy	1378	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1437
Db	1141	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1200
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1497
Db	1201	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1260
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGC	1557
Db	1261	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGC	1320
Qy	1558	TCATCTTGA	1566
Db	1321	TCATCTTGA	1329

RESULT 8

US-09-778-927A-27

; Sequence 27, Application US/09778927A

; Patent No. US20020068342A1

```

; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(800 )
; OTHER INFORMATION: n = a,c,g,t any unknown or other
US-09-778-927A-27

```

```

Query Match          17.7%; Score 763.2; DB 9; Length 800;
Best Local Similarity 98.3%; Pred. No. 1.9e-144;
Matches 771; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```

```

Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
      |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCGTGG 120
      |||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180
      |||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
      |||
Db    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300
      |||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
      |||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
      |||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
      |||

```

```

Db      421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
Qy      481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
Qy      541 TACATCAACACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TACATCAACACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA 600
Qy      601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
Qy      661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
Qy      721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780
        |||||||||||||||||||||||||||||||||||||||| || || || || || ||
Db      721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGCCAGGTAGGAGCGTTCACCCAC 780
Qy      781 AAAG 784
        ||
Db      781 CCAG 784

```

RESULT 9

US-09-962-436-531/c

; Sequence 531, Application US/09962436

; Patent No. US20020081301A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature Gene

; TITLE OF INVENTION: Sets

; FILE REFERENCE: 689290-75

; CURRENT APPLICATION NUMBER: US/09/962,436

; CURRENT FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/60/235,082

; PRIOR FILING DATE: 2000-09-25

; PRIOR APPLICATION NUMBER: US/60/234,924

; PRIOR FILING DATE: 2000-09-25

; NUMBER OF SEQ ID NOS: 568

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 531

; LENGTH: 592

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: n=a,t,g or c

US-09-962-436-531

```

Query Match      10.2%;  Score 440.6;  DB 9;  Length 592;
Best Local Similarity  90.1%;  Pred. No. 3.6e-79;
Matches  525;  Conservative  0;  Mismatches  47;  Indels  11;  Gaps  5;

```



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; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2060
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 H97587
; NAME/KEY: unsure
; LOCATION: (1)..(592)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-2060

```

```

Query Match          10.2%; Score 440.6; DB 10; Length 592;
Best Local Similarity 90.1%; Pred. No. 3.6e-79;
Matches 525; Conservative 0; Mismatches 47; Indels 11; Gaps 5;

```

```

Qy      993 GCGAATCTGCTTGCTTCATCCCGTTTCTGCTTGCCATTGGCCATCACTGCATTTTT 1052
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      578 GGGGAAGTGGCTGGCTCATCCNGTTTCTGCTTGCCATTGGCCATCACTGCATTTTT 521
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy      1053 AAAAGATTGGTGGCTGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTT 1112
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      520 CAAAAGATGGTGGCTGTCCAGTNC--AATTCCGGCTTTNCATGGCCATCACNGCA-TTTT 464
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy      1113 TTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAA 1172
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      463 TTATACACTAANGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAA 404
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy      1173 TG---ATCACCTAAAGCAGAGACGGGAAGTGGCCAAAA---CCGTCTTTTGCCTGGTCCT 1226
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      403 TGGACCACCCTAAAGCCAGAGCCGNAAGTGGCCAAAANCCGGTCTTTTGCCTGGTCCT 344
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy      1227 TGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTA 1286
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      343 GGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTA 284
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy      1287 TAATCAGAATGATCCCAATAGATGTGAACTTTTCTGTTGGTATTGGACTATAT 1346
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      283 TAATCAGAATGATCCCAATAGATGTGAACTTTTCTGTTGGTATTGGACTATAT 224
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy      1347 TGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAG 1406
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      223 TGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAG 164
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy      1407 CAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGA 1466
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      163 CAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGA 104
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy      1467 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATA 1526
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      103 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATA 44
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy      1527 TGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG 1569
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Db 43 TGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG 1

RESULT 11

US-09-954-531-917/c

; Sequence 917, Application US/09954531

; Patent No. US20020165180A1

; GENERAL INFORMATION:

; APPLICANT: Weaver, Zoe

; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer

; TITLE OF INVENTION: Gene Sets

; FILE REFERENCE: 689290-77

; CURRENT APPLICATION NUMBER: US/09/954,531

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: US/60/233,133

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US/60/234,009

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: US/60/234,034

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: US/60/234,509

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: US/60/234,567

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 1392

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 917

; LENGTH: 592

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(592)

; OTHER INFORMATION: n=a,t,g or c

US-09-954-531-917

Query Match 10.2%; Score 440.6; DB 10; Length 592;

Best Local Similarity 90.1%; Pred. No. 3.6e-79;

Matches 525; Conservative 0; Mismatches 47; Indels 11; Gaps 5;

```
Qy      993 GCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGC 1052
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      578 GGGGAACTGGCTGGCTCATCCNGTTCAGAAGACAGCTTNCAGCCAG--TTNCCAGGCCGG 521

Qy     1053 AAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTT 1112
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      520 CAAAAGATGGTGGCTGTCCAGTNC--AATTCCGGCTTTNCATGGCCATCACNGCA-TTTT 464

Qy     1113 TTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAA 1172
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      463 TTATACACTAANGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAA 404

Qy     1173 TG---ATCACCTAAAGCAGAGACGGGGAAGTGGCCAAAA---CCGTCTTTTGCCCTGGTCCT 1226
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      403 TGGACCACCTAAAGCCAGAGCCGGNAAGTGGCCAAAAANCCGGTCTTTTGCCCTGGTCCT 344
```

Qy 1227 TGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTA 1286  
 |||  
 Db 343 GGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTA 284

Qy 1287 TAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATAT 1346  
 |||  
 Db 283 TAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATAT 224

Qy 1347 TGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAG 1406  
 |||  
 Db 223 TGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAG 164

Qy 1407 CAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGA 1466  
 |||  
 Db 163 CAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGA 104

Qy 1467 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATA 1526  
 |||  
 Db 103 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATA 44

Qy 1527 TGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG 1569  
 |||  
 Db 43 TGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG 1

# RESULT 12

US-09-918-995-7311

; Sequence 7311, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 7311

; LENGTH: 405

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-918-995-7311

Query Match 9.4%; Score 403.4; DB 11; Length 405;

Best Local Similarity 99.8%; Pred. No. 9.9e-72;

Matches 404; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2062 TAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCATTTTTTCGGACACTGGAAACATT 2121  
 |||  
 Db 1 TAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCATTTTTTCGGACACTGGAAACATT 60

Qy 2122 TAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTTTTTGAAAATCATTACACTTT 2181  
 |||  
 Db 61 TAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTTTTTGAAAATCATTACACTTT 120



Qy 2182 CACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAACCAACATGTCACAAACAAGCAG 2241  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 CACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAACCAACATGTCACAAACAAGCAG 180

Qy 2242 CATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAATATAATACTTTTAAAAAGAAA 2301  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 CATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAATATAATACTTTTAAAAAGAAA 240

Qy 2302 ATTATTACATCCTTTACATTAGTTAAGATCAAACCTCACAAAGAGAAATAGAATGTTTG 2361  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 ATTATTACATCCTTTACATTAGTTAAGATCAAACCTCACAAAGAGAAATAGAATGTTTG 300

Qy 2362 AAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTCACATACCCTGTGAAGACAATAC 2421  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 AAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTCACATACCCTGTGAAGACAATAC 360

Qy 2422 TATCTACAATTTTTTTCAGGATTATTTAAATCTTCTTTTTTCACTA 2466  
 |||||||||||||||||||||||||||||||||||||||| ||||||||  
 Db 361 TATCTACAATTTTTTTCAGGATTATTTAAATCTTCTTTTTCACTA 405

RESULT 13

US-09-931-157-1  
 ; Sequence 1, Application US/09931157  
 ; Patent No. US20020082414A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Imura, Hiroo  
 ; APPLICANT: Nakao, Kazuwa  
 ; APPLICANT: Nakanishi, Shigetada  
 ; TITLE OF INVENTION: Human Endothelin Receptor  
 ; FILE REFERENCE: 299002032411  
 ; CURRENT APPLICATION NUMBER: US/09/931,157  
 ; CURRENT FILING DATE: 2001-10-15  
 ; PRIOR APPLICATION NUMBER: 08/121,446  
 ; PRIOR FILING DATE: 1993-09-14  
 ; PRIOR APPLICATION NUMBER: 07/911,684  
 ; PRIOR FILING DATE: 1992-07-10  
 ; PRIOR APPLICATION NUMBER: JP 3-172828  
 ; PRIOR FILING DATE: 1991-07-12  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4105  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (485)...(1768)  
 ; NAME/KEY: sig\_peptide  
 ; LOCATION: (485)...(544)  
 ; NAME/KEY: mat\_peptide  
 ; LOCATION: (545)...(1768)  
 US-09-931-157-1

Query Match 9.2%; Score 395.8; DB 9; Length 4105;  
 Best Local Similarity 65.7%; Pred. No. 1.3e-69;

Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      689 TGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Qy      565 CTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACACTTCTGAGAATTATCTACAAGAAC 624
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808

Qy      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 868

Qy      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928

Qy      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTCAGAAAGTCCTCG 988

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
      ||||| ||||| | | | | | | | | | | | | | | | | | | | |
Db      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048

Qy      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1049 TCCTGGAGTCGTGTTCAGGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCC 1108

Qy      910 ATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCCTGAAGCCATAGGTTTTGATATAATTACG 969
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1109 ATCTGGATCCTGTCTTTTATCCTGGCCATTTCCTGAAGCGATTGGCTTCGTTCATGGTACCC 1168

Qy      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT 1029
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222

Qy      1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTTG 1089
      ||||| ||||| ||||| | | | | | | | | | | | | | | | | | |
Db      1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCCTATTTCTGTATG 1282

Qy      1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1146
      || ||||| | | | | | | | | | | | | | | | | | | | | |
Db      1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342

Qy      1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402

Qy      1207 ACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG 1266
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1403 ACAGTTTTTCTGCTTGGTTGTAAATTTTGTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT 1462

Qy      1267 ATTCTGAAGCTCACTCTTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTT 1326
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1463 ATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522
```

Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1523 TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC 1582

Qy 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGC 1446  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642

Qy 1447 TGGTG 1451  
 | | |  
 Db 1643 TGCTG 1647

# RESULT 14

US-10-007-926A-229

; Sequence 229, Application US/10007926A  
 ; Publication No. US20030143539A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BERTUCCI, FRANCOIS  
 ; APPLICANT: HOULGATTE, REMI  
 ; APPLICANT: BIRNBAUM, DANIEL  
 ; APPLICANT: NGUYEN, CATHERINE  
 ; APPLICANT: VIENS, PATRICE  
 ; APPLICANT: FERT, VINCENT  
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS  
 ; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES  
 ; FILE REFERENCE: 1546-R-00  
 ; CURRENT APPLICATION NUMBER: US/10/007,926A  
 ; CURRENT FILING DATE: 2001-12-07  
 ; PRIOR APPLICATION NUMBER: 60/254,090  
 ; PRIOR FILING DATE: 2000-12-08  
 ; NUMBER OF SEQ ID NOS: 468  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 229  
 ; LENGTH: 4105  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: endothelin receptor type a (EDNRA) gene.  
 US-10-007-926A-229

Query Match 9.2%; Score 395.8; DB 13; Length 4105;  
 Best Local Similarity 65.7%; Pred. No. 1.3e-69;  
 Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

Qy 505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 689 TGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Qy 565 CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 749 ACTATTTTCATCGTGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTACCAGAAC 808

Qy 625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868

Qy	685	CACATCGTCATTGACATCCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	740
Db	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Qy	741	-----ATTTGGAGCTGAGATGTGTAAAGCTGGTGCCTTTCATACAGAAAGCCTCC	789
Db	929	GATCACAAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCAGAGAAGTCCTCG	988
Qy	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Db	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC	1048
Qy	850	TCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Db	1049	TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCCTTTGGTAAGTCCATTGAAATTGTCTCC	1108
Qy	910	ATTTGGGTGGTCTCTGTGTTTCTGGCTGTCCCTGAAGCCATAGGTTTGTATATAATTACG	969
Db	1109	ATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCC	1168
Qy	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCCGTTCAGAAGACAGCT	1029
Db	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Qy	1030	TTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG	1089
Db	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG	1282
Qy	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAG	1146
Db	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Qy	1147	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1206
Db	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCCAAA	1402
Qy	1207	ACCGTCTTTTGCCTGGTCCTTGCTTTGCCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG	1266
Db	1403	ACAGTTTCTGCTTGGTTGTAATTTTGTCTTTGCTCTTGGCTGGTTCCTCTTCACTTAAGCCGT	1462
Qy	1267	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT	1326
Db	1463	ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Qy	1327	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1386
Db	1523	TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC	1582
Qy	1387	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACTGCTTTAAGTCATGCTTATGCTGC	1446
Db	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCAGTCATGCCTCTGCTGC	1642
Qy	1447	TGGTG 1451	
Db	1643	TGCTG 1647	

RESULT 15

US-10-101-510-370

; Sequence 370, Application US/10101510  
 ; Publication No. US20030148295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WAN, JACKSON  
 ; APPLICANT: WANG, YIXIN  
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE  
 ; FILE REFERENCE: 15117.0012  
 ; CURRENT APPLICATION NUMBER: US/10/101,510  
 ; CURRENT FILING DATE: 2002-03-20  
 ; PRIOR APPLICATION NUMBER: 60/276,947  
 ; PRIOR FILING DATE: 2001-03-20  
 ; NUMBER OF SEQ ID NOS: 805  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 370  
 ; LENGTH: 4105  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-101-510-370

Query Match 9.2%; Score 395.8; DB 13; Length 4105;  
 Best Local Similarity 65.7%; Pred. No. 1.3e-69;  
 Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

Qy	505	TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC	564
Db	689	TGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT	748
Qy	565	CTTGTGTTCGTGCTGGGGATCATCGGGAAGTCCACACTTCTGAGAATTATCTACAAGAAC	624
Db	749	ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTACCAGAAC	808
Qy	625	AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	684
Db	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC	868
Qy	685	CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	740
Db	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Qy	741	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC	789
Db	929	GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAGTCCTCG	988
Qy	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Db	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC	1048
Qy	850	TCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Db	1049	TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Qy	910	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Db	1109	ATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTATGGTACCC	1168

Qy 970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT 1029  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222

Qy 1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTTG 1089  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282

Qy 1090 CCATTGGCCATCACTGCATTTTTTTTATACTAATGACCTGTGAAATGTTG--AGAAAG 1146  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342

Qy 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402

Qy 1207 ACCGTCCTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGG 1266  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1403 ACAGTTTTCTGCTTGGTTGTAATTTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462

Qy 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT 1326  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1463 ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522

Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1523 TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC 1582

Qy 1387 ATTGCTCTGTATTTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1446  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642

Qy 1447 TGGTG 1451  
 | | |  
 Db 1643 TGCTG 1647

Search completed: December 13, 2003, 00:41:45  
 Job time : 1270.7 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:16:56 ; Search time 995.175 Seconds  
(without alignments)  
11666.569 Million cell updates/sec

Title: US-09-931-157-2  
Perfect score: 4301  
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:\*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:\*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:\*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:\*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:\*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:\*
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- 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:\*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:\*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	%		Query		DB		ID	Description
No.	Score	Match	Length	DB	ID			
1	4297.8	99.9	4301	14	AAQ34584			ETb receptor gene.
2	4284.4	99.6	4286	21	AAF21284			Human low adenosin
3	4284.4	99.6	4286	21	AAA35162			Human adenosine re
4	4284.4	99.6	4286	24	ABV94186			Breast carcinoma r
5	4284.4	99.6	4286	25	ABZ42661			Human endothelin B
6	4284.4	99.6	13611	21	AAF21288			Human low adenosin
7	4284.4	99.6	13612	21	AAA35166			Human adenosine re
8	2857	66.4	2972	24	ABK94410			DNA encoding endot
c 9	2841.8	66.1	183337	25	ABQ77402			Human EDNRB DNA.
10	1691.8	39.3	1873	19	AAV17875			Homo sapiens endot
11	1690.8	39.3	1872	21	AAF21283			Human low adenosin
12	1690.8	39.3	1872	21	AAA35161			Human adenosine re
13	1495.4	34.8	1719	21	AAF21285			Human low adenosin
14	1495.4	34.8	1720	21	AAA35163			Human adenosine re
15	1466.8	34.1	1470	25	ACA56605			Human signalling p
16	1389	32.3	1632	24	AAD24966			Human G-protein co
17	1322.6	30.8	1329	23	ABI97988			Non-endogenous hum
18	1248	29.0	1578	25	ABX74409			Human cDNA sequenc
19	1220.4	28.4	1578	21	AAF21287			Human low adenosin
20	1220.4	28.4	1578	21	AAA35165			Human adenosine re
21	1099.2	25.6	1958	24	ABI99321			Mouse ischaemic co
22	1091	25.4	1965	13	AAQ25892			Sequence encodes e
23	1066	24.8	1406	15	AAQ53922			Bovine ET receptor
24	763.2	17.7	800	24	ABS51841			Novel human thromb
25	537.2	12.5	1752	24	ABK94409			DNA encoding endot
c 26	440.6	10.2	592	24	ABN95562			Gene #2060 used to
c 27	440.6	10.2	592	24	ABL63647			Breast cancer rela
c 28	440.6	10.2	592	24	ABL64653			Stomach cancer rel
29	395.8	9.2	1284	15	AAQ63209			Human endothelin r
30	395.8	9.2	1868	21	AAF20903			Human low adenosin
31	395.8	9.2	1868	21	AAF20915			Human endothelin r
32	395.8	9.2	1868	21	AAA34781			Human adenosine re
33	395.8	9.2	1868	21	AAA34793			Human adenosine re
34	395.8	9.2	2008	21	AAF20904			Human low adenosin
35	395.8	9.2	2008	21	AAA34782			Human adenosine re
36	395.8	9.2	4079	25	ACA56659			Human signalling p
37	395.8	9.2	4105	14	AAQ34583			ETa receptor gene.
38	395.8	9.2	4105	24	ABZ35259			Human gene express
39	395.8	9.2	4105	24	ABV94238			Breast carcinoma r
40	395.8	9.2	4105	25	ABZ42662			Human endothelin A
41	395.8	9.2	5036	21	AAF21447			Human endothelin r
42	395.8	9.2	117609	21	AAF21435			Human receptor-rel
43	395.4	9.2	4105	21	AAA38341			Human endothelin r
44	394.2	9.2	1310	21	AAF20902			Human endothelin r
45	394.2	9.2	1310	21	AAF20914			Human ELAM-1 polyn

# ALIGNMENTS



RESULT 1

AAQ34584

ID AAQ34584 standard; DNA; 4301 BP.

XX

AC AAQ34584;

XX

DT 25-MAR-2003 (updated)

DT 11-MAY-1993 (first entry)

XX

DE ETb receptor gene.

XX

KW Human; ETa; ETb; endothelin; receptor; transmembrane domain; N tail;

KW extracellular; cytoplasmic; C tail; post translational; bovine;

KW modification; ET-1 receptor; antagonist; circulatory system; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	238..1566
FT		/*tag= a
FT	sig_peptide	238..315
FT		/*tag= b
FT	mat_peptide	316..1563
FT		/*tag= c
FT	polyA_signal	2595..2600
FT		/*tag= d
FT	polyA_signal	3134..3139
FT		/*tag= e
FT	polyA_signal	3638..3643
FT		/*tag= f
FT	polyA_signal	4101..4106
FT		/*tag= g
FT	polyA_signal	4258..4263
FT		/*tag= h
FT	misc_feature	1909..1913
FT		/*tag= i
FT		/function= Related with mRNA instability
FT	misc_feature	1997..2001
FT		/*tag= j
FT		/function= Related with mRNA instability
FT	misc_feature	2119..2123
FT		/*tag= k
FT		/function= Related with mRNA instability
FT	misc_feature	2273..2277
FT		/*tag= l
FT		/function= Related with mRNA instability
FT	misc_feature	2745..2749
FT		/*tag= m
FT		/function= Related with mRNA instability
FT	misc_feature	3346..3350
FT		/*tag= n
FT		/function= Related with mRNA instability
FT	misc_feature	3484..3488
FT		/*tag= o
FT		/function= Related with mRNA instability
FT	misc_feature	3495..3499

FT /\*tag= p  
 FT /function= Related with mRNA instability  
 FT misc\_feature 3632..3636  
 FT /\*tag= q  
 FT /function= Related with mRNA instability  
 FT misc\_feature 3852..3856  
 FT /\*tag= r  
 FT /function= Related with mRNA instability  
 FT misc\_feature 4108..4112  
 FT /\*tag= s  
 FT /function= Related with mRNA instability  
 FT misc\_feature 4213..4217  
 FT /\*tag= t  
 FT /function= Related with mRNA instability

XX

PN EP522868-A1.

XX

PD 13-JAN-1993.

XX

PF 10-JUL-1992; 92EP-0306347.

XX

PR 12-JUL-1991; 91JP-0172828.

XX

PA (SHIO ) SHIONOGI SEIYAKU KK.

XX

PI Imura H, Nakanishi S, Nakao K;

XX

DR WPI; 1993-010677/02.

DR P-PSDB; AAR30886.

XX

PT Human ETa and ETb endothelin receptors - for measuring endothelin  
 PT and screening for endothelin antagonists

XX

PS Claim 12; Fig 2; 39pp; English.

XX

CC The sequences given in AAQ34583-84 encode the human ETa and ETb  
 CC endothelin receptors respectively. ETa is a 427 amino acid protein  
 CC with a molecular weight of 48,726. ETb comprises 442 amino acids and  
 CC has a molecular weight of 49,629. ETa has a higher affinity for  
 CC endothelin (ET)-1 and ET-2, whereas ETb has no selectivity for ET-1,  
 CC ET-2 or ET-3. The receptors each contain seven transmembrane domains  
 CC and have an extracellular N tail and a cytoplasmic C tail. There are  
 CC several potential sites for post translational modification, these  
 CC sites are identical to those of bovine ET-1 receptor. ETa cDNA is  
 CC 91.2% homologous to bovine ET-1 receptor cDNA and ETb cDNA is 61.1%  
 CC homologous to that of bovine ETa-receptor. The receptor proteins are  
 CC useful as reagents for measuring the amount of ET or screening for  
 CC antagonists of the ET receptor when studying the circulatory system.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 4301 BP; 1342 A; 830 C; 815 G; 1314 T; 0 other;

Query Match 99.9%; Score 4297.8; DB 14; Length 4301;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4299; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Db	1		GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61		AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61		AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121		AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121		AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181		AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181		AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241		CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241		CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301		TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301		TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361		ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361		ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421		CTGGCGCGGTCTGTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421		CTGGCGCGGTCTGTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481		CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481		CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541		TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTCTGGGGATCATCGGGAACCTCCACA	600
Db	541		TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTCTGGGGATCATCGGGAACCTCCACA	600
Qy	601		CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601		CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661		AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661		AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721		CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721		CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781		AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781		AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841		GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900

Db	841	GCTGTTGCTTCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTGTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 	960
Db	901	ATTGTTTTGATTGTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 	1080
Db	1021	AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGCTCTTGGCCCTCTGCTGGCTTCCCCTTCACCTC 	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGCTCTTGGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCAATAGATGTGAACTTTTG 	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACTGCTTTAAGTCATGCTTA 	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA 	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT 	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT 	1740
Db	1681	TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740

Qy	1741	TTACGGCATGGAAAAGAAAAATCAGTGGGAATTAAGAAAAGCCTCGTTCGTGAAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAAGAAAAATCAGTGGGAATTAAGAAAAGCCTCGTTCGTGAAAAGCACTTAAT	1800
Qy	1801	TTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTC AATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTC AATTAATAT	2040
Qy	2041	TATCACA CTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACA CTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Db	2341	CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580

Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCCTTTCTTTTCATCTAGAGGCAAACTGCTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCCTTTCTTTTCATCTAGAGGCAAACTGCTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480

Db	3421	 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Db	3481	 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Qy	3541	TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	 TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAATTGCATTCAAGTGGCTT	3660
Db	3601	 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAATTGCATTCAAGTGGCTT	3660
Qy	3661	TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	 CAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	 AAAAAATTATATATCTGGGAGGATTTTTTGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAAAAA 4301	

Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAA 4301

RESULT 2

AAF21284

ID AAF21284 standard; DNA; 4286 BP.

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AC AAF21284;

XX

DT 14-MAR-2001 (first entry)

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DE Human low adenosine antisense oligonucleotide related sequence #2851.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.

XX

PD 26-OCT-2000.

XX

PF 24-MAR-2000; 2000WO-US08020.

XX

PR 06-APR-1999; 99US-0127958.

XX

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX

PI Nyce JW;

XX

DR WPI; 2000-679539/66.

XX

PT Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -

XX

PS Disclosure; Page 1273-1274; 1592pp; English.

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CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and



CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
 CC and/or surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention.

XX

SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 other;

Query Match 99.6%; Score 4284.4; DB 21; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Db	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480

Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGA	600
Db	541	TACATCAACACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGA	600
Qy	601	CTTCTGAGAATTATCTACAAGAAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320

Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGGCTTCACTGAATTCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATCTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATCTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACTCTACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAATATTAAGTGTAATTATTTTAACTCTACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAAAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAAAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTCACTAGAGCCCAACCTCAGCATTCTGCAATATGTAAC	2220

Db	2161	 TTTTGAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	 CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	2281	 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	2341	 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	 CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	 GCAGGTAGCACCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	 TAAAGCTTATTACTAATTTTTTGATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	 AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAA CGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAA CGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060

Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900

Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286

# RESULT 3

AAA35162

ID AAA35162 standard; DNA; 4286 BP.

XX

AC AAA35162;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:36.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

XX

PR 03-AUG-1998; 98US-0095212.

Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020



Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021		
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081		
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141		
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201		
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261		
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321		
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Db	1381		
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441		
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501		
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561		
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621		
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681		
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741		
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801		
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860

Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTGTGCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTGTGCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760

Db	2701	 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	 CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACATGTGGCCA	3300
Db	3241	 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	 GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	 ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Db	3481	 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600

Db	3541	TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA	4200
Db	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286

RESULT 4

ABV94186

ID ABV94186 standard; cDNA; 4286 BP.

XX

AC ABV94186;

XX

DT 08-JAN-2003 (first entry)  
 XX  
 DE Breast carcinoma related nucleotide sequence SEQ ID NO:177.  
 XX  
 KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour;  
 KW gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200246467-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 07-DEC-2001; 2001WO-IB02811.  
 XX  
 PR 08-DEC-2000; 2000US-254090P.  
 PR 07-DEC-2001; 2001US-0007926.  
 XX  
 PA (IPSO-) IPSOGEN.  
 XX  
 PI Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;  
 XX  
 DR WPI; 2002-619023/66.  
 XX  
 PT Novel polynucleotide library useful in molecular characterization of a  
 PT carcinoma, comprising a pool of polynucleotide sequences or its  
 PT subsequences which are either underexpressed or overexpressed in tumor  
 PT cells -  
 XX  
 PS Claim 1; Page 225-226; 401pp; English.  
 XX  
 CC The present invention describes a polynucleotide library (I) useful in  
 CC the molecular characterisation of a carcinoma, comprising a pool of  
 CC polynucleotides or its subsequences which are either underexpressed or  
 CC overexpressed in tumour cells, and correspond to any of the  
 CC polynucleotide sequences chosen from the 468 sequences given in ABV94010  
 CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for  
 CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting  
 CC (M1) differentially expressed polynucleotide sequences which are  
 CC correlated with a cancer, involves obtaining a polynucleotide sample from  
 CC a patient, and reacting the polynucleotide sample obtained with a probe  
 CC immobilised on a solid support, where the probe comprises any combination  
 CC of the polynucleotide sequences of (I) or its expression products encoded  
 CC by polynucleotide sequences of (I), and detecting the reaction product.  
 CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)  
 CC is useful in molecular characterisation of a carcinoma. (I) and (II) are  
 CC useful for the prognosis or diagnostic of tumour, in differentiating a  
 CC normal cell from a cancer cell, detecting a hormone sensitive tumour  
 CC cell, differentiating a tumour with lymph nodes from a tumour without  
 CC lymph nodes, differentiating antracycline-sensitive tumours from  
 CC antracycline-insensitive tumours, and classifying good and poor prognosis  
 CC primary breast tumours. (I) is useful for large-scale molecular  
 CC characterisation of breast cancer that help in prediction, prognosis and  
 CC cancer treatment, and for detecting differentially expressed genes that  
 CC correlated with a cancer.  
 XX  
 SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 other;

Query Match 99.6%; Score 4284.4; DB 24; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Db	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780

Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTTGCAATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTTGCAATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680

Db	1621	 AACAAAATGAAACATTTGCCAAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	 TAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	 TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Db	1861	 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACCTGTAAACAGAACTTTTAAATG	1980
Db	1921	 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACCTGTAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTAATCAATTTTAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT	2040
Db	1981	 AAGCTTAAATTAATCAATTTTAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACAATATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	 TATCACAATATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	 TTTTGAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTCA	2400
Db	2341	 CAAAGAGAAATAGAATGTTTGAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAACTTCTTTTT	2460
Db	2401	 CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAACTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520



Db	2461	TCACATATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAAATACTATTTTTCAAATCATAAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAAATACTATTTTTCAAATCATAAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTTCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTTCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360

Qy	3361	ACAAACTTGTTCTTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCGCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCGCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTACTGCTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCAGAGTTTATTAA	3480
Db	3421	CATTTTACTGCTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCAGAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAAATTATTGTTAATCATGGATGTTA	3840
Db	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAAATTATTGTTAATCATGGATGTTA	3840
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 ||||||||||||||||||||||||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 5

ABZ42661

ID ABZ42661 standard; DNA; 4286 BP.

XX

AC ABZ42661;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human endothelin B receptor nucleotide SEQ ID NO:113.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US50107.

XX

PR 19-DEC-2000; 2000US-257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR P-PSDB; ABP81815.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating  
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
 PT cancer or autoimmune diseases -

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising:

CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino

CC acids. Also described: (1) an assay for the detection of a particular  
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity  
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and  
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting  
 CC an antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention.

XX

SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 other;

Query Match 99.6%; Score 4284.4; DB 25; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Db	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61	AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420

Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTTGTCTTGTGCTGCTGGGGATCATCGGGAACTCCACA	600
Db	541	TACATCAACACGGTTGTGTCTTGTCTTGTGCTGCTGGGGATCATCGGGAACTCCACA	600
Qy	601	CTTCTGAGAAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTTCACCTC	1260

Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160

Db	2101	 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	 TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	 CAACATGTCAAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA	2340
Db	2281	 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	2341	 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	 CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGAGTGTCCACATGACAAAGGG	2640
Db	2581	 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCTCTCTCACCCTGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	 GCAGGTAGCACCTCTCTCACCCTGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	 TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCTAGAGGCAAACTGCTTTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTCTAGAGGCAAACTGCTTTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	 AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000

Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAAATTCACACCCATATGGATTCTATTTATAAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAAATTCACACCCATATGGATTCTATTTATAAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAAAATGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAAAATGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAAATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAAATGT	3780
Qy	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840



Qy	3841	CAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286

# RESULT 6

AAF21288

ID AAF21288 standard; DNA; 13611 BP.

XX

AC AAF21288;

XX

DT 14-MAR-2001 (first entry)

XX

DE Human low adenosine antisense oligonucleotide related sequence #2855.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.  
 XX  
 PD 26-OCT-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US08020.  
 XX  
 PR 06-APR-1999; 99US-0127958.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX  
 PI Nyce JW;  
 XX  
 DR WPI; 2000-679539/66.  
 XX  
 PT Low adenosine (A) content antisense oligonucleotides which do not  
 PT trigger adenosine receptors during metabolism, useful e.g. for treating  
 PT cancers and respiratory obstructions -  
 XX  
 PS Disclosure; Page 1277-1280; 1592pp; English.  
 XX  
 CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
 CC and/or surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention.  
 XX  
 SQ Sequence 13611 BP; 3676 A; 3007 C; 3056 G; 3868 T; 4 other;  
  
 Query Match 99.6%; Score 4284.4; DB 21; Length 13611;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGACATTCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60  
 |||  
 Db 1873 GAGACATTCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 1932

Qy 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
 |||  
 Db 1933 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 1992

Qy 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180  
 |||  
 Db 1993 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 2052

Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 |||  
 Db 2053 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 2112

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
 |||  
 Db 2113 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 2172

Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
 |||  
 Db 2173 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 2232

Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
 |||  
 Db 2233 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 2292

Qy 421 CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
 |||  
 Db 2293 CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 2352

Qy 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA 540  
 |||  
 Db 2353 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA 2412

Qy 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA 600  
 |||  
 Db 2413 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA 2472

Qy 601 CTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||  
 Db 2473 CTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 2532

Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||  
 Db 2533 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 2592

Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780  
 |||  
 Db 2593 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 2652

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 2653 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 2712

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Db	2713	 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	2772
Qy	901	ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	2773	 ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	2832
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	2833	 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	2892
Qy	1021	AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	2893	 AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	2952
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	2953	 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	3012
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	3013	 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	3072
Qy	1201	GCCAAAACCGTCTTTTGCTGGTCCCTTGCTCTTTGCCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	3073	 GCCAAAACCGTCTTTTGCTGGTCCCTTGCTCTTTGCCCCTCTGCTGGCTTCCCCTTCACCTC	3132
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	3133	 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	3192
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	3193	 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	3252
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Db	3253	 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	3312
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	3313	 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	3372
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	3373	 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	3432
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA	1620
Db	3433	 TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA	3492
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	3493	 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	3552
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740

Db	3553	TAAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	3612
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	3613	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	3672
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	3673	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	3732
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	3733	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	3792
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	1980
Db	3793	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	3852
Qy	1981	AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT	2040
Db	3853	AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT	3912
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	3913	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	3972
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	3973	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	4032
Qy	2161	TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	4033	TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	4092
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	4093	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	4152
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	4153	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	4212
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA	2400
Db	4213	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA	4272
Qy	2401	CATACCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	4273	CATACCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	4332
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	4333	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	4392
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	4393	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	4452

Qy	2581	GCCAGTGCCTCATAATAAAGACTGTGAACTGCCTGGTGCGAGTGTCCACATGACAAAGGG	2640
Db	4453		
Qy	2641	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCGAGTGTCCACATGACAAAGGG	4512
Qy	2641	GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	4513		
Qy	2641	GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	4572
Qy	2701	GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	4573		
Qy	2701	GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	4632
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	4633		
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	4692
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT	2880
Db	4693		
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT	4752
Qy	2881	AGCTTTGTGCGTTTCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	4753		
Qy	2881	AGCTTTGTGCGTTTCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	4812
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	4813		
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	4872
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	4873		
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	4932
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	4933		
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	4992
Qy	3121	GAGTGACTTTTCAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA	3180
Db	4993		
Qy	3121	GAGTGACTTTTCAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA	5052
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	5053		
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	5112
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	5113		
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	5172
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Db	5173		
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	5232
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	5233		
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	5292

Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	5293	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	5352
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Db	5353	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	5412
Qy	3541	TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	5413	TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	5472
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT	3660
Db	5473	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT	5532
Qy	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	5533	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	5592
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	5593	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	5652
Qy	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	5653	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	5712
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	5713	CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	5772
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	5773	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	5832
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	5833	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	5892
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	5893	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	5952
Qy	4081	TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	5953	TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	6012
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTTAAAGAAATATAAATGTGA	4200
Db	6013	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTTAAAGAAATATAAATGTGA	6072
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	6073	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	6132
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286

|||||  
Db 6133 AAAATGCCACATTTCTGGTCTCTGGG 6158

RESULT 7

AAA35166

ID AAA35166 standard; DNA; 13612 BP.

XX

AC AAA35166;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:40.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

XX

PR 03-AUG-1998; 98US-0095212.

XX

PA (UYEC-) UNIV EAST CAROLINA.

XX

PI Nyce JW;

XX

DR WPI; 2000-205971/18.

XX

PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers -

XX

PS Disclosure; Page 1194-1197; 1343pp; English.

XX

CC The present invention describes a new composition comprising an  
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive



CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of  
CC the ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
CC differ from the previously named sequences. SEQ ID NO:11 to 1680  
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present  
CC invention. N.B. Sequences given in the disclosure of the present  
CC invention do not match up with their corresponding SEQ ID NO: sequences  
CC given in the sequence listing.

SQ Sequence 13612 BP; 3677 A; 3007 C; 3056 G; 3868 T; 4 other;

Query Match 99.6%; Score 4284.4; DB 21; Length 13612;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAA CGTGGATCCTGAGAGCACTCCC 60  
 |||  
 Db 1873 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAA CGTGGATCCTGAGAGCACTCCC 1932

QY 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
 |||||  
 Db 1933 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 1992

Qy 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180  
 |||||  
 Db 1993 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 2052

Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 |||||  
 Db 2053 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 2112

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCCTGCGCTGCGGCCTG 300  
 |||||  
 Db 2113 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCCTGCGCTGCGGCCTG 2172

Qy            301 TCGCGGATCTGGGGAGAGGAGAGAGGCCTCCCGCCTGACAGGGCCA CTCCGCTTTTGCAA       360  
                 |||||  
Db            2173 TCGCGGATCTGGGGAGAGGAGAGAGGCCTCCCGCCTGACAGGGCCA CTCCGCTTTTGCAA       2232

Qy            361 ACCGCAGAGATAATGACGCCACCCTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT      420  
               |||||  
Db            2233 ACCGCAGAGATAATGACGCCACCCTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT      2289

Qy 421 CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
 |||||  
 Db 2293 CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 2352

Qy 481 CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
| | | | |  
Db 2353 CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 2412

Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA	600
Db	2413	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA	2472
Qy	601	CTTCTGAGAATTATCTACAAGAACAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	2473	CTTCTGAGAATTATCTACAAGAACAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	2532
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	2533	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	2592
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	2593	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	2652
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	2653	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	2712
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	2713	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	2772
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGCTGTCCTGAAGCCATAGGTTTTGAT	960
Db	2773	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGCTGTCCTGAAGCCATAGGTTTTGAT	2832
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	2833	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	2892
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	2893	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	2952
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	2953	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	3012
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	3013	AGAAAGAAAAGTGGCATGCAGATTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	3072
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	3073	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	3132
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAAATGATCCCAATAGATGTGAACTTTTG	1320
Db	3133	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAAATGATCCCAATAGATGTGAACTTTTG	3192
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	3193	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	3252
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440

Db	3253	 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA	3312
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	3313	 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	3372
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	3373	 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	3432
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	3433	 TCTTGAAAGAAGAACTATTCACTGTATTTCATTTTCTTTATATTGGACCGAAGTCATTAA	3492
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGCTATGTATTTGCACAGCACACTAT	1680
Db	3493	 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGCTATGTATTTGCACAGCACACTAT	3552
Qy	1681	TAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	3553	 TAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	3612
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	3613	 TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	3672
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	3673	 TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	3732
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	3733	 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	3792
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	3793	 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	3852
Qy	1981	AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Db	3853	 AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTTTCAATTAATAT	3912
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	3913	 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	3972
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	3973	 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	4032
Qy	2161	TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	4033	 TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC	4092
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280

Db	4093	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	4152
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	4153	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	4212
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	4213	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	4272
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	4273	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	4332
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	4333	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	4392
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	4393	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	4452
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	4453	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	4512
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	4513	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	4572
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATAAGATTAGTACATTTAACAGCTACCTG	2760
Db	4573	GCTATAGTTAAAATACTATTTTTTCAAATCATAAGATTAGTACATTTAACAGCTACCTG	4632
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	4633	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	4692
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT	2880
Db	4693	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT	4752
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	4753	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	4812
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	4813	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	4872
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	4873	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	4932
Qy	3061	CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	4933	CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	4992

Qy	3121	GAGTGACTTTCGAAATAAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	4993	GAGTGACTTTCGAAATAAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	5052
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	5053	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	5112
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	5113	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	5172
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	5173	GAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTTATAAATCACCC	5232
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	5233	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	5292
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTACAGTTTATTAA	3480
Db	5293	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTACAGTTTATTAA	5352
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Db	5353	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	5412
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	5413	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	5472
Qy	3601	TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTCAAGTGGCTT	3660
Db	5473	TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTCAAGTGGCTT	5532
Qy	3661	TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	5533	TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	5592
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	5593	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	5652
Qy	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	5653	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	5712
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	5713	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	5772
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	5773	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	5832

Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAATATAACAATGT	4020
Db	5833	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAATATAACAATGT	5892
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	5893	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	5952
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC	4140
Db	5953	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC	6012
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA	4200
Db	6013	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA	6072
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	6073	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	6132
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	6133	AAAATGCCACATTTCTGGTCTCTGGG	6158

RESULT 8

ABK94410

ID ABK94410 standard; DNA; 2972 BP.

XX

AC ABK94410;

XX

DT 27-AUG-2002 (first entry)

XX

DE DNA encoding endothelin receptor B (EDNRB), exon 7.

XX

KW Endothelin; EDN; endothelin converting enzyme; ECE; EDNRB;  
 KW endothelin receptor B; signaling system; cardiovascular disease;  
 KW coronary heart disease; hypertension; atherosclerosis; angiogenesis;  
 KW fatty acid metabolism; diabetes; familial hypercholesterolaemia;  
 KW forensic marker; transgenic animal; solid support; SNP;  
 KW cardiovascular regulator; gene; ds; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	variation	replace(1048,A)
FT		/*tag= a
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	replace(1658,C)
FT		/*tag= b
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	replace(1912,T)
FT		/*tag= c
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	replace(2130,T)
FT		/*tag= d
FT		/standard_name= "Single nucleotide polymorphism"

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XX
PN WO200224747-A2.
XX
PD 28-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-EP10087.
XX
PR 19-SEP-2000; 2000EP-0120123.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Brinkmann U, Hoffmeyer S;
XX
DR WPI; 2002-435060/46.
XX
PT Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme
PT signaling system associated with cardiovascular disease, useful for
PT treating the disease -
XX
PS Claim 1; Page -; 190pp; English.
XX
CC The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC a molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of
CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC signaling system or its gene product. The isolated proteins and
CC polynucleotides encoding them are useful for preparation of a
CC pharmaceutical composition for treating a cardiovascular disease such as
CC coronary heart disease, hypertension, atherosclerosis, or related to
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC creating a transgenic animal and in creation of a solid support
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC host cells of the invention. This sequence encodes a fragment of the
CC cardioavascular regulator Endothelin receptor B (EDNRB).
CC Note: This sequence does not appear in the specification but has been
CC obtained from GenBank using information given in the invention.
XX
SQ Sequence 2972 BP; 1018 A; 499 C; 465 G; 990 T; 0 other;

Query Match          66.4%;  Score 2857;  DB 24;  Length 2972;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 2857;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy 1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 68

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Qy	1490	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATA	1549
Db	69	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATA	128
Qy	1550	AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACC	1609
Db	129	AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACC	188
Qy	1610	GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA	1669
Db	189	GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA	248
Qy	1670	CAGCACACTATTAAAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATT	1729
Db	249	CAGCACACTATTAAAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATT	308
Qy	1730	TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA	1789
Db	309	TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA	368
Qy	1790	AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT	1849
Db	369	AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT	428
Qy	1850	CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG	1909
Db	429	CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG	488
Qy	1910	ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA	1969
Db	489	ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA	548
Qy	1970	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAACAACTTT	2029
Db	549	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAACAACTTT	608
Qy	2030	TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	2089
Db	609	TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	668
Qy	2090	AGTTGTTGCATTTTTTCGGACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAAG	2149
Db	669	AGTTGTTGCATTTTTTCGGACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAAG	728
Qy	2150	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTTCTG	2209
Db	729	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTTCTG	788
Qy	2210	CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	2269
Db	789	CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	848
Qy	2270	TGAATTTAAAAATATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTCACTTAAG	2329
Db	849	TGAATTTAAAAATATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTCACTTAAG	908



Qy	2330	ATCAAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAAGACTTTTTTTGAA	2389
Db	909		
		ATCAAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAAGACTTTTTTTGAA	968
Qy	2390	TCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	2449
Db	969		
		TCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	1028
Qy	2450	ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	2509
Db	1029		
		ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	1088
Qy	2510	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	2569
Db	1089		
		ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	1148
Qy	2570	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	2629
Db	1149		
		GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	1208
Qy	2630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGC	2689
Db	1209		
		ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGC	1268
Qy	2690	ATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACATTTA	2749
Db	1269		
		ATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACATTTA	1328
Qy	2750	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	2809
Db	1329		
		ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	1388
Qy	2810	AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	2869
Db	1389		
		AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	1448
Qy	2870	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT	2929
Db	1449		
		AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT	1508
Qy	2930	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAG	2989
Db	1509		
		TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAG	1568
Qy	2990	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT	3049
Db	1569		
		GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT	1628
Qy	3050	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG	3109
Db	1629		
		CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG	1688
Qy	3110	CAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	3169
Db	1689		
		CAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	1748
Qy	3170	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA	3229

Db	1749	GCCCCAAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA	1808
Qy	3230	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA	3289
Db	1809	GCCCCAAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA	1868
Qy	3290	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	3349
Db	1869	GCCCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	1928
Qy	3350	ATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	3409
Db	1929	ATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	1988
Qy	3410	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	3469
Db	1989	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	2048
Qy	3470	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACT	3529
Db	2049	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACT	2108
Qy	3530	GAATTTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	3589
Db	2109	GAATTTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	2168
Qy	3590	TTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCA	3649
Db	2169	TTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCA	2228
Qy	3650	TTCAGTGGCTTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA	3709
Db	2229	TTCAGTGGCTTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA	2288
Qy	3710	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	3769
Db	2289	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	2348
Qy	3770	TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	3829
Db	2349	TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	2408
Qy	3830	CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	3889
Db	2409	CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	2468
Qy	3890	CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	3949
Db	2469	CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	2528
Qy	3950	AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	4009
Db	2529	AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	2588
Qy	4010	TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	4069
		TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	

Db 2589 TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA 2648  
 Qy 4070 GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACATA 4129  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2649 GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACATA 2708  
 Qy 4130 CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 4189  
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 Db 2709 CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 2768  
 Qy 4190 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 4249  
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 Db 2769 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 2828  
 Qy 4250 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 4286  
 ||||||||||||||||||||||||||||||||||||||||||  
 Db 2829 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 2865

RESULT 9

ABQ77402/c

ID ABQ77402 standard; DNA; 183337 BP.

XX

AC ABQ77402;

XX

DT 10-MAY-2003 (first entry)

XX

DE Human EDNRB DNA.

XX

KW Human; EDNRB; vascular disease; cardiant; antiarteriosclerotic; stroke;  
 KW cerebroprotective; gene therapy; coronary artery disease; ischaemia;  
 KW myocardial infarction; peripheral vascular disease; pulmonary embolism;  
 KW venous thromboembolism; forensic; paternity testing; GI12597038; gene;  
 KW SNP; single nucleotide polymorphism; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT variation replace (75672,t)

FT /\*tag= a

FT /standard\_name= "SNP"

FT /note= "Single nucleotide polymorphism (ID G337a4)

FT which does not change the EDNBR protein"

XX

PN WO2003016494-A2.

XX

PD 27-FEB-2003.

XX

PF 16-AUG-2002; 2002WO-US26343.

XX

PR 16-AUG-2001; 2001US-313097P.

PR 05-OCT-2001; 2001US-327485P.

PR 14-DEC-2001; 2001US-0020141.

XX

PA (VITI-) VITIVITY INC.

XX

PI McCarthy J, Ableson A;

XX  
DR WPI; 2003-300617/29.  
DR P-PSDB; ABG74670.  
XX  
PT Identifying a subject as a candidate for a particular course of therapy  
PT to treat a vascular disease or disorder, e.g. stroke, myocardial  
PT infarction or ischemia by determining the identity of the nucleotide  
PT present at specific positions -  
XX  
PS Claim 1; Fig 5; 568pp; English.  
XX  
CC This invention describes a novel method for identifying a subject as a  
CC candidate for a particular course of therapy to treat a vascular disease  
CC or disorder. The method comprises determining the identity of the  
CC nucleotide present at specific positions, or their complements, and  
CC identifying the subject as a candidate for a particular clinical course  
CC of therapy based on the identity of the nucleotide present in that  
CC specific position. The method can be used for identifying a subject who  
CC is a candidate for further diagnostic evaluation of a vascular disease or  
CC disorder and selecting a clinical course of therapy. The products of the  
CC invention have cardiant, antiarteriosclerotic and cerebroprotective  
CC activity and can be used for gene therapy. The methods disclosed are  
CC useful for treating a vascular disease, e.g. atherosclerosis, coronary  
CC artery disease, myocardial infarction, ischaemia, stroke, peripheral  
CC vascular diseases, venous thromboembolism and pulmonary embolism. The DNA  
CC sequences are useful as fingerprint for detecting different individuals  
CC within the same species applicable in forensic studies and paternity  
CC testing. This sequence encodes the human EDNBR gene represented in  
CC GI12597038, used to illustrate the method of the invention.  
XX  
SQ Sequence 183337 BP; 56451 A; 33595 C; 34663 G; 58628 T; 0 other;

Query Match 66.1%; Score 2841.8; DB 25; Length 183337;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2854; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	1430	AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC	1489
Db	72830	AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC	72771
Qy	1490	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA	1549
Db	72770	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA	72711
Qy	1550	AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACC	1609
Db	72710	AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACC	72651
Qy	1610	GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAAACAAAACAAAAAATATGTATTTGCA	1669
Db	72650	GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAAACAAAACAAAAAATATGTATTTGCA	72591
Qy	1670	CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT	1729
Db	72590	CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT	72531
Qy	1730	TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA	1789

Db	72530	 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA	72471
Qy	1790	AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT	1849
Db	72470	 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT	72411
Qy	1850	CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG	1909
Db	72410	 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG	72351
Qy	1910	ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA	1969
Db	72350	 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA	72291
Qy	1970	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTT	2029
Db	72290	 ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTT	72231
Qy	2030	TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	2089
Db	72230	 TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	72171
Qy	2090	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG	2149
Db	72170	 AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG	72111
Qy	2150	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTG	2209
Db	72110	 AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTG	72051
Qy	2210	CAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	2269
Db	72050	 CAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	71991
Qy	2270	TGAATTTAAATATAATACTTTTTAAAAGAAAATTATTACATCCTTTACATTAGTTAAG	2329
Db	71990	 TGAATTTAAATATAATACTTTTTAAAAGAAAATTATTACATCCTTTACATTAGTTAAG	71931
Qy	2330	ATCAAACCTCACAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA	2389
Db	71930	 ATCAAACCTCACAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA	71871
Qy	2390	TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	2449
Db	71870	 TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	71811
Qy	2450	ATCTTCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	2509
Db	71810	 ATCTTCTTCTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	71751
Qy	2510	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	2569
Db	71750	 ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	71691
Qy	2570	GATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	2629

Db	71690	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	71631
Qy	2630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC	2689
Db	71630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC	71571
Qy	2690	ATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAATCATAACAGATTAGTACATTTA	2749
Db	71570	ATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAATCATAACAGATTAGTACATTTA	71511
Qy	2750	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	2809
Db	71510	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	71451
Qy	2810	AAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	2869
Db	71450	AAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	71391
Qy	2870	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	2929
Db	71390	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	71331
Qy	2930	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	2989
Db	71330	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	71271
Qy	2990	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTT	3049
Db	71270	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTT	71211
Qy	3050	CGTCATTGCCTCGTCAATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTG	3109
Db	71210	CGTCATTGCCTCGTCAATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTG	71151
Qy	3110	CAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	3169
Db	71150	CAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	71091
Qy	3170	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGGCCACATGTTGGAAATA	3229
Db	71090	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGGCCACATGTTGGAAATA	71031
Qy	3230	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	3289
Db	71030	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	70971
Qy	3290	CAATGTGGCCAGAAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	3349
Db	70970	CAATGTGGCCAGAAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	70911
Qy	3350	ATAAATCACCCACAAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	3409
Db	70910	ATAAATCACCCACAAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	70851
Qy	3410	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	3469
Db	70850	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	70791

Qy	3470	CAGTTTATTATAATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	3529
Db	70790	CAGTTTATTATAATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	70731
Qy	3530	GAATTTTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	3589
Db	70730	GAATTTTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	70671
Qy	3590	TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCA	3649
Db	70670	TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCA	70611
Qy	3650	TTCAGTGGCTTTTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAA	3709
Db	70610	TTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAA	70552
Qy	3710	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	3769
Db	70551	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	70492
Qy	3770	TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTAA	3829
Db	70491	TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTAA	70432
Qy	3830	CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	3889
Db	70431	CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	70372
Qy	3890	CCACTGCTAATGTGGATGTATGTTCAAAACCTTTTAGTATTGATAGCTTACATATGGCC	3949
Db	70371	CCACTGCTAATGTGGATGTATGTTCAAAACCTTTTAGTATTGATAGCTTACATATGGCC	70312
Qy	3950	AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	4009
Db	70311	AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	70252
Qy	4010	TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	4069
Db	70251	TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	70192
Qy	4070	GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTA	4129
Db	70191	GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTA	70132
Qy	4130	CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA	4189
Db	70131	CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA	70072
Qy	4190	TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA	4249
Db	70071	TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA	70012
Qy	4250	GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	4286
Db	70011	GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	69975

RESULT 10

AAV17875

ID AAV17875 standard; cDNA to mRNA; 1873 BP.

XX

AC AAV17875;

XX

DT 03-AUG-1998 (first entry)

XX

DE Homo sapiens endothelin B receptor gene.

XX

KW dystroglycan; hDG; progressive muscular dystrophy;

KW endothelin B receptor; alpha-sarcoglycan; Hirschsprung's disease; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 44..1204

FT /\*tag= a

FT /product= dystroglycan

XX

PN EP825265-A1.

XX

PD 25-FEB-1998.

XX

PF 14-AUG-1997; 97EP-0114019.

XX

PR 16-AUG-1996; 96JP-0216506.

XX

PA (RIKA ) INST PHYSICAL & CHEM RES.

PA (RIKA ) RIKAGAKU KENKYUSHO.

XX

PI Hanaoka F, Sakamoto A;

XX

DR WPI; 1998-132258/13.

XX

PT cDNA reverse transcription and amplification - using different

PT reverse transcription and 3' amplification primers

XX

PS Example 3; Page 19-21; 25pp; English.

XX

CC The sequence is that encoding human endothelin B receptor which is

CC implicated in Hirschsprung's disease.

XX

SQ Sequence 1873 BP; 490 A; 434 C; 438 G; 511 T; 0 other;

Query Match 39.3%; Score 1691.8; DB 19; Length 1873;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1696; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237  
|| || |||||

Db 171 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 230

Qy 238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297  
|||

Db 231 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 290



Qy	298	CTGTCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTTGACAGGGCCACTCCGCTTTTG	357
Db	291	CTGTGCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTTGACAGGGCCACTCCGCTTTTG	350
Qy	358	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	417
Db	351	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	410
Qy	418	AGTCTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	477
Db	411	AGTCTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	470
Qy	478	CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	537
Db	471	CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	530
Qy	538	AAATACATCAACACGGTTGTGTCTTGCTTGTGTTCTGCTGTTGGGGATCATCGGGAACTCC	597
Db	531	AAATACATCAACACGGTTGTGTCTTGCTTGTGTTCTGCTGTTGGGGATCATCGGGAACTCC	590
Qy	598	ACACTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATC	657
Db	591	ACACTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATC	650
Qy	658	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	717
Db	651	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	710
Qy	718	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	777
Db	711	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	957
Db	891	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	1011	CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTATTCAGTTTC	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130

Qy	1138	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
Db	1251	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1310
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1370
Qy	1378	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAGATTCAAAAAGTCTTTAAGTCATGC	1437
Db	1371	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAGATTCAAAAAGTCTTTAAGTCATGC	1430
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1497
Db	1431	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1490
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1557
Db	1491	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1550
Qy	1558	TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT	1617
Db	1551	TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT	1610
Qy	1618	TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1677
Db	1611	TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1670
Qy	1678	TATTAAAATATTAAGTGTAATTATTTTAAACTCACAGCTACATATGACATTTTATGAGC	1737
Db	1671	TATTAAAATATTAAGTGTAATTATTTTAAACTCACAGCTACATATGACATTTTATGAGC	1730
Qy	1738	TGTTTACGGCATGGAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1797
Db	1731	TGTTTACGGCATGGAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1790
Qy	1798	AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC	1857
Db	1791	AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC	1850
Qy	1858	ACTTAGGCTTAAAAATGAGCTCA	1880
Db	1851	ACTTAGGCTTAAAAATGAGCTCA	1873

RESULT 11

AAF21283

ID AAF21283 standard; DNA; 1872 BP.

XX

AC AAF21283;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Human low adenosine antisense oligonucleotide related sequence #2850.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200062736-A2.  
XX  
PD 26-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US08020.  
XX  
PR 06-APR-1999; 99US-0127958.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-679539/66.  
XX  
PT Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -  
XX  
PS Disclosure; Page 1273; 1592pp; English.  
XX  
CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The



Db	711	AAGCTGCTGGCAGAGGACTGGCCATTTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTT	957
Db	891	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	1011	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTATTTCAGTTTC	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
Db	1251	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1310
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1370
Qy	1378	ATTAACCCCAATTGCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGTCTTTAAGTCATGC	1437
Db	1371	ATTAACCCCAATTGCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGTCTTTAAGTCATGC	1430
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1497
Db	1431	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1490
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1557
Db	1491	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1550
Qy	1558	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT	1617
Db	1551	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT	1610

Qy 1618 TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC 1677  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1611 TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC 1670

Qy 1678 TATTAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGC 1737  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1671 TATTAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGC 1730

Qy 1738 TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1797  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1731 TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1790

Qy 1798 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1857  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1791 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1850

Qy 1858 ACTTAGGCTTAAAAATGAGCTC 1879  
 ||||||||||||||||||||  
 Db 1851 ACTTAGGCTTAAAAATGAGCTC 1872

RESULT 12

AAA35161

ID AAA35161 standard; DNA; 1872 BP.

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AC AAA35161;

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DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:35.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

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PR 03-AUG-1998; 98US-0095212.

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PA (UYEC-) UNIV EAST CAROLINA.

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PI Nyce JW;

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DR WPI; 2000-205971/18.

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Db	411	AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	470
Qy	478	CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTC	537
Db	471	CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTC	530
Qy	538	AAATACATCAACACGGTTGTGTCTGCTTGTGTTCGTGCTGGGGATCATCGGGAACTCC	597
Db	531	AAATACATCAACACGGTTGTGTCTGCTTGTGTTCGTGCTGGGGATCATCGGGAACTCC	590
Qy	598	ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC	657
Db	591	ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC	650
Qy	658	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	717
Db	651	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	710
Qy	718	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	777
Db	711	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAAATGGACAGCAGTA	897
Db	831	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	957
Db	891	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	1011	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTATTTCAGTTTC	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAAATG	1130
Qy	1138	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
Db	1251	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1310



Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1370
Qy	1378	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1437
Db	1371	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1430
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1497
Db	1431	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1490
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGC	1557
Db	1491	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGC	1550
Qy	1558	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTCTTTATATTGGACCGAAGTCAT	1617
Db	1551	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTCTTTATATTGGACCGAAGTCAT	1610
Qy	1618	TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACAC	1677
Db	1611	TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACAC	1670
Qy	1678	TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1737
Db	1671	TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1730
Qy	1738	TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1797
Db	1731	TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1790
Qy	1798	AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC	1857
Db	1791	AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC	1850
Qy	1858	ACTTAGGCTTAAAAATGAGCTC	1879
Db	1851	ACTTAGGCTTAAAAATGAGCTC	1872

# RESULT 13

AAF21285

ID AAF21285 standard; DNA; 1719 BP.

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AC AAF21285;

XX

DT 14-MAR-2001 (first entry)

XX

DE Human low adenosine antisense oligonucleotide related sequence #2852.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KW human; airway disorder; bronchoconstriction; lung inflammation;

KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;

KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;

KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.

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OS Homo sapiens.

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PN WO200062736-A2.

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PD 26-OCT-2000.

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PF 24-MAR-2000; 2000WO-US08020.

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PR 06-APR-1999; 99US-0127958.

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PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

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PI Nyce JW;

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DR WPI; 2000-679539/66.

XX

PT Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -

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PS Disclosure; Page 1274-1275; 1592pp; English.

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CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
CC and/or surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of

CC the present invention.

XX

SQ Sequence 1719 BP; 444 A; 400 C; 412 G; 463 T; 0 other;

Query Match 34.8%; Score 1495.4; DB 21; Length 1719;  
Best Local Similarity 99.8%; Pred. No. 2.5e-303;  
Matches 1503; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	203	GCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCG	262
Db	200	GCGGCCACCGGACG-CTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCG	258
Qy	263	GACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTGGGGAGAGGAGA	322
Db	259	GACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTGGGGAGAGGAGA	318
Qy	323	GAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCCAC	382
Db	319	GAGGCTTCCCGCCCGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCCAC	378
Qy	383	CCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTGCTTGGCACCTG	442
Db	379	CCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTGCTTGGCACCTG	438
Qy	443	CGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCC	502
Db	439	CGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCC	498
Qy	503	CGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCT	562
Db	499	CGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCT	558
Qy	563	GCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGA	622
Db	559	GCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGA	618
Qy	623	ACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGC	682
Db	619	ACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGC	678
Qy	683	TGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCAT	742
Db	679	TGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCAT	738
Qy	743	TTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTG	802
Db	739	TTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTG	798
Qy	803	TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA	862
Db	799	TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA	858
Qy	863	TTAAAGGAATTGGGGTTCCAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCT	922
Db	859	TTAAAGGAATTGGGGTTCCAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCT	918
Qy	923	CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG	982

Db	919	 CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG	978
Qy	983	GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTTCATGCAGTTTT	1042
Db	979	 GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTTCATGCAGTTTT	1038
Qy	1043	ACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA	1102
Db	1039	 ACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA	1098
Qy	1103	CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGA	1162
Db	1099	 CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGA	1158
Qy	1163	TTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG	1222
Db	1159	 TTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG	1218
Qy	1223	TCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC	1282
Db	1219	 TCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC	1278
Qy	1283	TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT	1342
Db	1279	 TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT	1338
Qy	1343	ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG	1402
Db	1339	 ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG	1398
Qy	1403	TGAGCAAAAGATTCAAAAACGCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTG	1462
Db	1399	 TGAGCAAAAGATTCAAAAACGCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTG	1458
Qy	1463	AAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACG	1522
Db	1459	 AAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACG	1518
Qy	1523	GATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAAGAACTATTAC	1582
Db	1519	 GATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAAGAACTATTAC	1578
Qy	1583	TGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAACAAAATGAAACATTTGCCAA	1642
Db	1579	 TGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAACAAAATGAAACATTTGCCAA	1638
Qy	1643	AACAAAACAAAAACTATGTATTTGCACAGCACACTATTAAATATTAAGTGTAATTATT	1702
Db	1639	 AACAAAACAAAAACTATGTATTTGCACAGCACACTATTAAATATTAAGTGTAATTATT	1698
Qy	1703	TTAACA 1708 	
Db	1699	TTAAAA 1704	

AAA35163

ID AAA35163 standard; DNA; 1720 BP.

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AC AAA35163;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:37.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

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OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

XX

PR 03-AUG-1998; 98US-0095212.

XX

PA (UYEC-) UNIV EAST CAROLINA.

XX

PI Nyce JW;

XX

DR WPI; 2000-205971/18.

XX

PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers -

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PS Disclosure; Page 1192; 1343pp; English.

XX

CC The present invention describes a new composition comprising an  
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of  
CC the ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing

CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
CC differ from the previously named sequences. SEQ ID NO:11 to 1680  
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present  
CC invention. N.B. Sequences given in the disclosure of the present  
CC invention do not match up with their corresponding SEQ ID NO: sequences  
CC given in the sequence listing.

XX

SQ Sequence 1720 BP; 445 A; 400 C; 412 G; 463 T; 0 other;

Query Match 34.8%; Score 1495.4; DB 21; Length 1720;  
Best Local Similarity 99.8%; Pred. No. 2.5e-303;  
Matches 1503; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	203	GCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCG	262
Db	200	GCGGCCACCGGACG-CTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCG	258
Qy	263	GACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTGGGGAGAGGAGA	322
Db	259	GACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTGGGGAGAGGAGA	318
Qy	323	GAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCCAC	382
Db	319	GAGGCTTCCCGCCCGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCCAC	378
Qy	383	CCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTCTGTGGCACCTG	442
Db	379	CCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTCTGTGGCACCTG	438
Qy	443	CGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCC	502
Db	439	CGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCC	498
Qy	503	CGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCT	562
Db	499	CGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCT	558
Qy	563	GCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGA	622
Db	559	GCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGA	618
Qy	623	ACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGC	682
Db	619	ACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGC	678
Qy	683	TGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCAT	742
Db	679	TGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCAT	738
Qy	743	TTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTG	802
Db	739	TTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTG	798
Qy	803	TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA	862

Db	799	 TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA	858
Qy	863	TTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCT	922
Db	859	 TTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCT	918
Qy	923	CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG	982
Db	919	 CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG	978
Qy	983	GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTT	1042
Db	979	 GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTT	1038
Qy	1043	ACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA	1102
Db	1039	 ACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA	1098
Qy	1103	CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGA	1162
Db	1099	 CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGA	1158
Qy	1163	TTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG	1222
Db	1159	 TTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG	1218
Qy	1223	TCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC	1282
Db	1219	 TCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC	1278
Qy	1283	TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT	1342
Db	1279	 TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT	1338
Qy	1343	ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG	1402
Db	1339	 ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG	1398
Qy	1403	TGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTG	1462
Db	1399	 TGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTG	1458
Qy	1463	AAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACG	1522
Db	1459	 AAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACG	1518
Qy	1523	GATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAAGAACTATTAC	1582
Db	1519	 GATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAAGAACTATTAC	1578
Qy	1583	TGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAAACAAAATGAAACATTTGCCAA	1642
Db	1579	 TGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAAACAAAATGAAACATTTGCCAA	1638
Qy	1643	AACAAAACAAAAACTATGTATTTGCACAGCACACTATTAATAATTAAGTGTAATTATT	1702

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Db      1639 AACAAAACAAAAA ACTATGTATTTGCACAGCACACTATTAAAATATTAAGTGTAAATTATT 1698
Qy      1703 TTAACA 1708
        |||||
Db      1699 TTAAAA 1704

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# RESULT 15

ACA56605

ID ACA56605 standard; cDNA; 1470 BP.

XX

AC ACA56605;

XX

DT 06-JUN-2003 (first entry)

XX

DE Human signalling pathway polynucleotide probe SEQ ID NO 1203.

XX

KW Human; probe; ss; array element; Parkinson's disease;

KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

XX

OS Homo sapiens.

XX

PN US6500938-B1.

XX

PD 31-DEC-2002.

XX

PF 30-JAN-1998; 98US-0016434.

XX

PR 30-JAN-1998; 98US-0016434.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Au-Young J, Seilhamer JJ;

XX

DR WPI; 2003-352189/33.

XX

PT Combination of polynucleotide probes, useful as array elements in a

PT microarray for monitoring the expression of a number of target

PT polynucleotides -

XX

PS Claim 1; SEQ ID NO 1203; 65pp; English.

XX

CC The invention relates to a combination which, comprises a number of  
 CC polynucleotide probes comprising a sequence selected from one of the 1490  
 CC sequences mentioned in the specification. The combination is useful as an  
 CC array element in a microarray for monitoring the expression of a number  
 CC of target polynucleotides. The microarray is particularly useful in the  
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.  
 CC The microarray is useful in diagnostics and treatment regimens, drug  
 CC discovery and development, toxicological and carcinogenicity studies,  
 CC forensics and pharmacogenomics. The microarray is also useful for  
 CC monitoring progression of diseases and for developing sophisticated  
 CC profiles for the effects of currently available therapeutic drugs. The  
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
 CC and genomic fragments and in research and diagnostic applications. The  
 CC array can detect changes in expression in a large number of genes coding



CC for different signaling pathway populations which can be used to diagnose  
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,  
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
CC and Parkinson's disease. The present sequence represents a polynucleotide  
CC probe of the invention.

CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format directly from USPTO  
CC at [seqdata.uspto.gov/sequence.html?DocID=06500938B1](http://seqdata.uspto.gov/sequence.html?DocID=06500938B1).

XX

SQ Sequence 1470 BP; 381 A; 343 C; 350 G; 396 T; 0 other;

Query Match 34.1%; Score 1466.8; DB 25; Length 1470;  
Best Local Similarity 99.9%; Pred. No. 2.3e-297;  
Matches 1468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      192 GAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC 251
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Db      1  GAAACTGCGGACGGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC 60

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Db      61 AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTG 120

Qy      312 GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT 371
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Db      121 GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT 180

Qy      372 AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC 431
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Db      181 AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC 240

Qy      432 GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT 491
          |||
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Qy      492 CTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC 551
          |||
Db      301 CTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC 360

Qy      552 GGTGTGTCTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAAT 611
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Db      361 GGTGTGTCTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAAT 420

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Db      481 GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA 540

Qy      732 GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT 791
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Db      541 GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT 600

Qy      792 GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC 851
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Db	601	GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTTGCTTC	660
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Db	661	TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAAATGGACAGCAGTAGAAAATTGTTTTGAT	720
Qy	912	TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT	971
Db	721	TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT	780
Qy	972	GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT	1031
Db	781	GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT	840
Qy	1032	CATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTTGCC	1091
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Qy	1092	ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG	1151
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Qy	1392	TCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTG	1451
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Job time : 1006.18 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:16:57 ; Search time 15090.3 Seconds  
(without alignments)  
11659.930 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_ba:\*  
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 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	4301	100.0	4301	6	E07650		E07650	cDNA encodi
3	4286	99.7	4286	9	HUMETR		D90402	Homo sapien
4	4284.4	99.6	4286	6	AX548828		AX548828	Sequence
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c 9	2792.4	64.9	201093	2	AC144750		AC144750	Pan trogl
10	2610	60.7	2720	11	G06417		G06417	human STS W
c 11	2550	59.3	169751	2	AC130785		AC130785	Papio anu
c 12	2550	59.3	185870	2	AC129069		AC129069	Papio anu
13	1691.8	39.3	1873	6	AR165435		AR165435	Sequence
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16	1495.4	34.8	1719	9	HUMEDNRB		L06623	Homo sapien
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21	1361.4	31.7	1765	9	AF114165		AF114165	Homo sapi
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27	1186	27.6	1452	4	AF034530		AF034530	Canis fam
28	1113	25.9	2018	10	S65355		S65355	nonselectiv
29	1110.2	25.8	1551	6	E05930		E05930	DNA sequenc
30	1104.8	25.7	2115	10	BC026553		BC026553	Mus muscu
31	1099.2	25.6	1958	6	AX305434		AX305434	Sequence
32	1099.2	25.6	1958	10	MMU32329		U32329	Mus musculu
33	1091	25.4	1892	10	RNETBREC		X57764	Rat mRNA fo

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35	1086.6	25.3	1311	4	AF038900	AF038900 Equus cab
36	1070.4	24.9	1321	6	AR207426	AR207426 Sequence
37	1067.6	24.8	1314	4	AF276427	AF276427 Canis fam
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c 41	922.2	21.4	192330	2	AC122157	AC122157 Canis fam
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44	588	13.7	588	11	G15922	G15922 human STS C
45	564.8	13.1	1520	5	AF275636	AF275636 Danio rer

# ALIGNMENTS

## RESULT 1

AR177880

LOCUS AR177880 4301 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 3 from patent US 6313276.

ACCESSION AR177880

VERSION AR177880.1 GI:17920235

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 4301)

AUTHORS Imura,H., Nakao,K. and Nakanishi,S.

TITLE Human endothelin receptor

JOURNAL Patent: US 6313276-A 3 06-NOV-2001;

FEATURES Location/Qualifiers

source 1..4301

/organism="unknown"

BASE COUNT 1342 a 828 c 817 g 1314 t

ORIGIN

Query Match 100.0%; Score 4301; DB 6; Length 4301;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Db	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240

Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
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Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
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Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
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Qy	841	GCTGTTGCTTCTTGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
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Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
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Qy	1021	AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
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Db	1081	 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
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Db	1141	 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	 GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
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Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
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Db	1981	AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT	2040
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Qy	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
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Qy	3601	TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
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## RESULT 2

E07650

LOCUS E07650 4301 bp RNA linear PAT 29-SEP-1997

DEFINITION cDNA encoding endothelin receptor, ETB-receptor.

ACCESSION E07650

VERSION E07650.1 GI:2175785

KEYWORDS JP 1994157595-A/2.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4301)

AUTHORS Imura,H., Nakao,I. and Nakanishi,S.  
 TITLE HUMAN ENDOTHELIN RECEPTOR  
 JOURNAL Patent: JP 1994157595-A 2 03-JUN-1994;  
 SHIONOGI & CO LTD  
 COMMENT OS Homo sapiens (human)  
 PN JP 1994157595-A/2  
 PD 03-JUN-1994  
 PF 12-JUL-1991 JP 1991172828  
 PI IMURA HIROO, NAKAO ICHIKAZU, NAKANISHI SHIGETADA PC  
 C07K13/00,C12N5/10,C12N15/12,C12P21/02,(C12N5/10,C12R1:91), PC  
 (C12P21/02,  
 PC C12R1:91);  
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 BASE COUNT 1342 a 828 c 817 g 1314 t  
 ORIGIN

Query Match 100.0%; Score 4301; DB 6; Length 4301;  
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 Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 |||

Db 3841 CAGCTCAAAGATTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 |||

Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 |||

Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 |||

Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTTC 4140  
 |||

Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 |||

Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||

Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301  
 |||

Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301

# RESULT 3

## HUMETR

LOCUS HUMETR 4286 bp mRNA linear PRI 18-DEC-2002

DEFINITION Homo sapiens ETR mRNA for endothelin receptor, complete cds.

ACCESSION D90402

VERSION D90402.1 GI:219651

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Db	481	CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Qy	541	TACATCAACACGGTTGTGTCTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCCACA	600
Db	541	TACATCAACACGGTTGTGTCTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCCACA	600
Qy	601	CTTCTGAGAAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG	1020

Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACCTGAATTCCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACCTGAATTCCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860

Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTTAAATTTTAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTTAAATTTTAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCTAGTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCTAGTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCTCTCTCACCCTATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCTCTCTCACCCTATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760

Db	2701	 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATGCCT	3060
Db	3001	 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATGCCT	3060
Qy	3061	CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	 CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Db	3481	 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600

Db	3541	TCCTGATACCCCTTCTCTTCTCCATGTCTAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	AAAAAATTATATATCTGGGAGGATTTTTTGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286

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Db	481	 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGA	600
Qy	601	CTTCTGAGAATTATCTACAAGAA	660
Db	601	CTTCTGAGAATTATCTACAAGAA	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTT	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTT	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTC	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTC	900
Qy	901	ATTGTTTTGATTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380

Db	1321	AGCTTTCTGTTGGTATTGGACTATATTTGGTATCAACATGGCTTCACTGAATTCCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAATATTTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAATATTTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGCGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGCGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACTTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAACACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAACACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAACCTCAGCATTCTGCAATATGTAAC	2220

Qy	2221	CAACATGTCAAAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAAA	2280
Db	2221	CAACATGTCAAAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAAA	2280
Qy	2281	TATAATACTTTTTAAAAAGAAAATTATTACATCCTTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTTAAAAAGAAAATTATTACATCCTTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAAATAGAATGTTTGTAAAGGCTATCCCAAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Db	2341	CAAAGAGAAAATAGAATGTTTGTAAAGGCTATCCCAAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCTCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTTT	2460
Db	2401	CATACCTCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
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Qy	2701	GCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
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Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
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Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
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Qy	3541	TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT	3660
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Db	3841	CAGCTCAAAAGATTTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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# RESULT 5

AX587707

LOCUS AX587707 4286 bp DNA linear PAT 10-JAN-2003

DEFINITION Sequence 177 from Patent WO0246467.

ACCESSION AX587707

VERSION AX587707.1 GI:28212378

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Bertucci,F., Houlgatte,R., Birnbaum,D., Nguyen,C., Viens,P. and Fert,V.

TITLE Gene expression profiling of primary breast carcinomas using arrays of candidate genes

JOURNAL Patent: WO 0246467-A 177 13-JUN-2002; Ipsogen (FR)

FEATURES Location/Qualifiers

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/note="primer"

misc\_feature 1. .4286  
/note="endothelin receptor type b (EDNRB) gene."

BASE COUNT 1327 a 829 c 816 g 1314 t

ORIGIN

Query Match 99.6%; Score 4284.4; DB 6; Length 4286;  
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Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

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Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
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Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
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Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACTTCCAGGATATTACACAACACT	1860
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Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACA CTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACA CTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
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Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
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Db	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
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Db	2341	CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATACTTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATACTTTCTTTTT	2460
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Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTGGTGTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580



Db	2521		CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581		GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581		GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
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Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
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 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 6

S57283

LOCUS S57283 4286 bp mRNA linear PRI 18-MAR-2002

DEFINITION Homo sapiens endothelin ET-B receptor mRNA, complete cds.

ACCESSION S57283

VERSION S57283.1 GI:298321

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4286)

AUTHORS Arai,H., Nakao,K., Hosoda,K., Ogawa,Y., Nakagawa,O., Komatsu,Y. and Imura,H.

TITLE Molecular cloning of human endothelin receptors and their expression in vascular endothelial cells and smooth muscle cells

JOURNAL Jpn. Circ. J. 56 Suppl 5, 1303-1307 (1992)

MEDLINE 93180293

PUBMED 1291713

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 128424] from the original journal article.  
 This sequence comes from Fig. 5.

FEATURES

source

Location/Qualifiers

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BASE COUNT 1327 a 829 c 816 g 1314 t

ORIGIN

Query Match 99.6%; Score 4284.4; DB 9; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60  
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Db	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900

Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740

Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACCTGTAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACCTGTAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTTGAAACATTTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTTGAAACATTTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640

Db	2581	 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTCAAATCATAAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAATACTATTTTTCAAATCATAAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
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Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
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Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
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Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCAGGTTTATTAA	3480

Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480

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Db 3541 TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600

Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAAGTGGCTT 3660  
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Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAAGTGGCTT 3660

Qy 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
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Db 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780  
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Db 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780

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Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

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Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
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Db 3901 GTGGATGTATGTTCAAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

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Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

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Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

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Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
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Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
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Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286



## RESULT 7

D13162S7

LOCUS D13162S7 2972 bp DNA linear PRI 12-OCT-2002

DEFINITION Homo sapiens hET-BR gene for endothelin-B receptor, complete cds and exon 7.

ACCESSION D13168

VERSION D13168.1 GI:285924

KEYWORDS .

SEGMENT 7 of 7

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2972)

AUTHORS Arai,H., Nakao,K., Takaya,K., Hosoda,K., Ogawa,Y., Nakanishi,S. and Imura,H.

TITLE The human endothelin-B receptor gene. Structural organization and chromosomal assignment

JOURNAL J. Biol. Chem. 268 (5), 3463-3470 (1993)

MEDLINE 93155196

PUBMED 8429023

REFERENCE 2 (bases 1 to 2972)

AUTHORS Arai,H.

TITLE Direct Submission

JOURNAL Submitted (02-SEP-1992) Hiroshi Arai, Kyoto University School of Medicine, Second Division, Department of Medicine; 54 Shogoin, Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan (Tel:81-75-751-3170, Fax:81-75-771-9452)

FEATURES Location/Qualifiers

source

1. .2972

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/db\_xref="taxon:9606"

/chromosome="13"

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D13167.1:11. .119,11. .2865)

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/note="G protein-coupled receptor"

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BASE COUNT    1018 a    499 c    465 g    990 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2857; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	2150	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTTCTG	2209
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Db	789	CAATATGTAACCAACATGTGCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	848
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Db	849	TGAATTTAAATATAAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG	908
Qy	2330	ATCAAACCTCACAAAGAGAAAATAGAAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTTGAA	2389
Db	909	ATCAAACCTCACAAAGAGAAAATAGAAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTTGAA	968
Qy	2390	TCTGTCAATTCACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA	2449
Db	969	TCTGTCAATTCACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA	1028
Qy	2450	ATCTTCTTTTTTTCCTATCGTAGCTTAAACTCTGTTTGGTTTTGTGCATCTGTAAATACCT	2509
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Qy	2510	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	2569
Db	1089	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	1148
Qy	2570	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCAC	2629
Db	1149	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCAC	1208
Qy	2630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGC	2689
Db	1209	ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGC	1268
Qy	2690	ATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA	2749
Db	1269	ATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA	1328
Qy	2750	ACAGCTACCTGTAAAGCTTATTACTAATTTTTTGTTATTATTTTTGTAAATAGCCAATAGAA	2809
Db	1329	ACAGCTACCTGTAAAGCTTATTACTAATTTTTTGTTATTATTTTTGTAAATAGCCAATAGAA	1388
Qy	2810	AAGTTTGCCTTGACATGGTGCCTTTTCTTTCATCTAGAGGCAAAACCTGCTTTTTTGAGACCGT	2869
Db	1389	AAGTTTGCCTTGACATGGTGCCTTTTCTTTCATCTAGAGGCAAAACCTGCTTTTTTGAGACCGT	1448
Qy	2870	AAGAACCTCTTAGCTTTTGTGCGTTCTCGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	2929
Db	1449	AAGAACCTCTTAGCTTTTGTGCGTTCTCGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	1508

Qy	2930	TAGGATAGCTTGGGATGAGATGTTGTGTGAAAAGTATGTACAAGAGAAAAACGGAAGAGAGAG	2989
Db	1509	TAGGATAGCTTGGGATGAGATGTTGTGTGAAAAGTATGTACAAGAGAAAAACGGAAGAGAGAG	1568
Qy	2990	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTT	3049
Db	1569	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTT	1628
Qy	3050	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG	3109
Db	1629	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG	1688
Qy	3110	CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	3169
Db	1689	CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	1748
Qy	3170	AATATGCCCAAATTTTTACTTTTGTCTTTTCTTTAATAGGCTGGGGCCACATGTTGGAAATA	3229
Db	1749	AATATGCCCAAATTTTTACTTTTGTCTTTTCTTTAATAGGCTGGGGCCACATGTTGGAAATA	1808
Qy	3230	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	3289
Db	1809	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	1868
Qy	3290	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	3349
Db	1869	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	1928
Qy	3350	ATAAATCACCCACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	3409
Db	1929	ATAAATCACCCACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	1988
Qy	3410	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	3469
Db	1989	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	2048
Qy	3470	CAGTTTATTAATATATTTTAAATTTCTATTTTAAATTTTGAATTATTTTTATTACCATGTACT	3529
Db	2049	CAGTTTATTAATATATTTTAAATTTCTATTTTAAATTTTGAATTATTTTTATTACCATGTACT	2108
Qy	3530	GAATTTTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	3589
Db	2109	GAATTTTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	2168
Qy	3590	TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA	3649
Db	2169	TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA	2228
Qy	3650	TTCAGTGGCTTTTTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAA	3709
Db	2229	TTCAGTGGCTTTTTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAA	2288
Qy	3710	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	3769
Db	2289	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	2348
Qy	3770	TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	3829

Db	2349		TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	2408
Qy	3830		CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	3889
Db	2409		CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	2468
Qy	3890		CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	3949
Db	2469		CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	2528
Qy	3950		AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	4009
Db	2529		AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	2588
Qy	4010		TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	4069
Db	2589		TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	2648
Qy	4070		GTTACTGATTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAATA	4129
Db	2649		GTTACTGATTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAATA	2708
Qy	4130		CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA	4189
Db	2709		CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA	2768
Qy	4190		TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA	4249
Db	2769		TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA	2828
Qy	4250		GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	4286
Db	2829		GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	2865

RESULT 8

AL139002/c

LOCUS AL139002 183337 bp DNA linear PRI 28-JAN-2001

DEFINITION Human DNA sequence from clone RP11-318G21 on chromosome 13q22.2-31.1, complete sequence.

ACCESSION AL139002

VERSION AL139002.18 GI:12597038

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 183337)

AUTHORS Wall,M.

TITLE Direct Submission

JOURNAL Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Jan 29, 2001 this sequence version replaced gi:12584355. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr13>

RP11-318G21 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

This sequence is the entire insert of clone RP11-318G21 The true left end of clone RP11-267I18 is at 125528 in this sequence.

FEATURES	Location/Qualifiers
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repeat_region	1216. .1308 /note="HAL1 repeat: matches 1475. .1563 of consensus"
repeat_region	1309. .1597 /note="AluJb repeat: matches 1. .297 of consensus"
repeat_region	1598. .2044 /note="HAL1 repeat: matches 1003. .1475 of consensus"
repeat_region	2148. .2276 /note="L2 repeat: matches 2620. .2749 of consensus"
repeat_region	2330. .2378 /note="L2 repeat: matches 2442. .2492 of consensus"
repeat_region	3915. .4224 /note="AluY repeat: matches 1. .306 of consensus"
repeat_region	4617. .4750 /note="67 copies 2 mer cc 61% conserved"
repeat_region	4648. .4727 /note="20 copies 4 mer cctt 78% conserved"
repeat_region	4729. .4784 /note="14 copies 4 mer tcct 78% conserved"
repeat_region	5431. .5736 /note="AluSx repeat: matches 1. .305 of consensus"
repeat_region	11990. .12273 /note="AluSx repeat: matches 9. .292 of consensus"

repeat_region	12589. .12809
	/note="MIR repeat: matches 7. .234 of consensus"
repeat_region	13390. .13519
	/note="L2 repeat: matches 2410. .2548 of consensus"
repeat_region	14630. .14978
	/note="THE1B repeat: matches 1. .360 of consensus"
repeat_region	15092. .15580
	/note="L1MB1 repeat: matches 5656. .6116 of consensus"
repeat_region	15581. .16095
	/note="L1PA7 repeat: matches 5629. .6143 of consensus"
repeat_region	16096. .16549
	/note="L1MB1 repeat: matches 5188. .5656 of consensus"
repeat_region	16731. .16777
	/note="MIR repeat: matches 35. .78 of consensus"
repeat_region	16778. .17137
	/note="THE1C repeat: matches 1. .371 of consensus"
repeat_region	17138. .17273
	/note="MIR repeat: matches 78. .226 of consensus"
repeat_region	17374. .17484
	/note="MIR repeat: matches 26. .158 of consensus"
repeat_region	17485. .17777
	/note="AluSc repeat: matches 1. .290 of consensus"
repeat_region	17778. .17815
	/note="MIR repeat: matches 158. .191 of consensus"
repeat_region	18981. .19048
	/note="34 copies 2 mer tt 66% conserved"
repeat_region	19447. .19589
	/note="MIR repeat: matches 131. .262 of consensus"
repeat_region	19843. .20162
	/note="MER33 repeat: matches 1. .324 of consensus"
repeat_region	20866. .21198
	/note="MER44A repeat: matches 3. .333 of consensus"
repeat_region	21742. .21878
	/note="MIR repeat: matches 9. .154 of consensus"
repeat_region	22214. .22310
	/note="MIR repeat: matches 164. .260 of consensus"
repeat_region	22321. .22418
	/note="L1MB8 repeat: matches 6078. .6171 of consensus"
misc_feature	22390. .22715
	/note="Sequence from AC018674 sequenced by WUGSC."
repeat_region	22419. .22730
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repeat_region	22731. .23714
	/note="L1MB8 repeat: matches 5130. .6078 of consensus"
repeat_region	23715. .24008
	/note="AluSg repeat: matches 1. .294 of consensus"
repeat_region	24009. .24264
	/note="L1MB8 repeat: matches 4884. .5130 of consensus"
repeat_region	24265. .24569
	/note="AluY repeat: matches 1. .305 of consensus"
repeat_region	24570. .25577
	/note="L1MB8 repeat: matches 3786. .4884 of consensus"
repeat_region	25582. .25635
	/note="27 copies 2 mer tt 70% conserved"
repeat_region	26221. .26571
	/note="MSTA repeat: matches 1. .347 of consensus"
repeat_region	26572. .26750

repeat_region	/note="AluY repeat: matches 129. .307 of consensus" 26752. .27066
repeat_region	/note="AluY repeat: matches 1. .311 of consensus" 27067. .27134
repeat_region	/note="MSTA repeat: matches 347. .371 of consensus" 27963. .28006
repeat_region	/note="22 copies 2 mer tt 75% conserved" 28916. .29282
repeat_region	/note="MER39 repeat: matches 13. .381 of consensus" 29282. .29517
repeat_region	/note="MER39b repeat: matches 327. .579 of consensus" 30210. .30526
repeat_region	/note="AluJo repeat: matches 1. .303 of consensus" 31423. .31572
repeat_region	/note="L1PA13 repeat: matches 6005. .6155 of consensus" 31587. .31624
repeat_region	/note="19 copies 2 mer tt 86% conserved" 32103. .32181
repeat_region	/note="ORSL repeat: matches 390. .467 of consensus" 33878. .34312
repeat_region	/note="MER57A repeat: matches 1. .433 of consensus" 36673. .36768
repeat_region	/note="LTR37A repeat: matches 81. .172 of consensus" 36769. .37066
repeat_region	/note="AluSq repeat: matches 1. .296 of consensus" 37067. .37300
repeat_region	/note="LTR37A repeat: matches 172. .424 of consensus" 39470. .39501
repeat_region	/note="16 copies 2 mer tt 90% conserved" 41434. .42607
repeat_region	/note="L1M4 repeat: matches -258. .888 of consensus" 42744. .43220
repeat_region	/note="L1M4 repeat: matches 1085. .1580 of consensus" 43703. .44007
repeat_region	/note="AluJb repeat: matches 1. .305 of consensus" 44019. .44180
repeat_region	/note="L1MD1 repeat: matches 6044. .6211 of consensus" 44183. .44485
repeat_region	/note="AluJo repeat: matches 1. .300 of consensus" 44486. .44611
repeat_region	/note="L1MD2 repeat: matches 5949. .6066 of consensus" 45256. .45430
repeat_region	/note="MER5B repeat: matches 1. .178 of consensus" 45588. .45669
repeat_region	/note="MER5A repeat: matches 109. .188 of consensus" 46919. .47084
repeat_region	/note="MIR repeat: matches 94. .260 of consensus" 47873. .47902
repeat_region	/note="15 copies 2 mer tg 90% conserved" 49906. .49933
repeat_region	/note="7 copies 4 mer tgtg 96% conserved" 50452. .50507
repeat_region	/note="LTR37A repeat: matches 128. .184 of consensus" 51786. .51829
repeat_region	/note="MER74A repeat: matches 271. .309 of consensus" 51830. .52172
	/note="THE1B repeat: matches 1. .364 of consensus"





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Db	72170	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG	72111
Qy	2150	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTG	2209
Db	72110	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTG	72051
Qy	2210	CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	2269
Db	72050	CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	71991
Qy	2270	TGAATTTAAATATAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG	2329
Db	71990	TGAATTTAAATATAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG	71931
Qy	2330	ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA	2389
Db	71930	ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA	71871
Qy	2390	TCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	2449
Db	71870	TCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	71811
Qy	2450	ATCTTCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	2509
Db	71810	ATCTTCTTCTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	71751
Qy	2510	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	2569
Db	71750	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	71691
Qy	2570	GATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	2629
Db	71690	GATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	71631
Qy	2630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAATGGTTTCTAGC	2689
Db	71630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAATGGTTTCTAGC	71571
Qy	2690	ATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTA	2749
Db	71570	ATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTA	71511
Qy	2750	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	2809
Db	71510	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	71451
Qy	2810	AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	2869
Db	71450	AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	71391
Qy	2870	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	2929
Db	71390	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	71331

Qy	2930	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	2989
Db	71330	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	71271
Qy	2990	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT	3049
Db	71270	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT	71211
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Db	71210	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG	71151
Qy	3110	CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	3169
Db	71150	CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	71091
Qy	3170	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA	3229
Db	71090	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA	71031
Qy	3230	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	3289
Db	71030	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	70971
Qy	3290	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	3349
Db	70970	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	70911
Qy	3350	ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	3409
Db	70910	ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	70851
Qy	3410	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	3469
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Qy	3470	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACT	3529
Db	70790	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACT	70731
Qy	3530	GAATTTTTTACATCCTGATACCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATC	3589
Db	70730	GAATTTTTTACATCCTGATACCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATC	70671
Qy	3590	TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA	3649
Db	70670	TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA	70611
Qy	3650	TTCAGTGGCTTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA	3709
Db	70610	TTCAGTGGCTTTTTT-AAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA	70552
Qy	3710	ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	3769
Db	70551	ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	70492

Qy 3770 TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA 3829  
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 Db 70491 TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA 70432

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 Db 70311 AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA 70252

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 Db 70191 GTTACTGATTTTTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACAATA 70132

Qy 4130 CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 4189  
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Qy 4190 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 4249  
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 Db 70071 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 70012

Qy 4250 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 4286  
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 Db 70011 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 69975

# RESULT 9

AC144750/c

LOCUS AC144750 201093 bp DNA linear HTG 04-JUN-2003

DEFINITION Pan troglodytes clone CH251-517B22, WORKING DRAFT SEQUENCE, 3 ordered pieces.

ACCESSION AC144750

VERSION AC144750.2 GI:31376422

KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 201093)

AUTHORS Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., Chu,G., Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R., Karlins,E., Kwong,P., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E.,

Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.

TITLE NISC Comparative Sequencing Initiative

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 201093)

AUTHORS Green,E.D.

TITLE Direct Submission

JOURNAL Submitted (15-MAY-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA

REFERENCE 3 (bases 1 to 201093)

AUTHORS Green,E.D.

TITLE Direct Submission

JOURNAL Submitted (04-JUN-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA

COMMENT On Jun 4, 2003 this sequence version replaced gi:30725907.

----- Genome Center

Center: NIH Intramural Sequencing Center

Center code: NISC

Web site: <http://www.nisc.nih.gov>

Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)

----- Project Information

Center project name: esg

Center clone name: 517B22

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 200649 bases at least Q40

Consensus quality: 200775 bases at least Q30

Consensus quality: 200836 bases at least Q20

Insert size: 165000; agarose-fp

Insert size: 200893; sum-of-contigs

Quality coverage: 13.47x in Q20 bases; agarose-fp

Quality coverage: 11.07x in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 3 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces

\* is believed to be correct as given, however the sizes

\* of the gaps between them are based on estimates that have

\* provided by the submittor.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.  
 \* 1 107546: contig of 107546 bp in length  
 \* 107547 107646: gap of unknown length  
 \* 107647 153000: contig of 45354 bp in length  
 \* 153001 153100: gap of unknown length  
 \* 153101 201093: contig of 47993 bp in length.

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 VERSION G06417.1 GI:859662  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2720)  
 AUTHORS Hudson,T.  
 TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
 Mapped ESTs  
 JOURNAL Unpublished (1995)  
 COMMENT  
 Contact: Thomas Hudson  
 Whitehead Institute/MIT Center for Genome Research  
 Whitehead Institute for Biomedical Research  
 9 Cambridge Center, Cambridge MA 02142 USA  
 Tel: 617 252 1900  
 Fax: 617 252 1902  
 Email: thudson@genome.wi.mit.edu  
  
 Primer A: ATGGAGAGATGCCAGTGACC  
 Primer B: TAGGCAGGAACGCACAAAG  
 STS size: 331  
 PCR Profile:  
 Presoak:  
 Denaturation:  
 Annealing: 56 degrees C  
 Polymerization:  
 PCR Cycles: 35  
 Thermal Cycler:  
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Qy       1867 TAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAATCAA 1926
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Qy	2827	TGCTTTTCTTTTCATCTAGAGGCAAACTGCCTTTTGTAGACCGTAAGAACCTCTTAGCTTT	2886
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Db	1381	AGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTGGGGTTG	1440
Qy	3007	GAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCTCGTCAC	3066
Db	1441	GAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCTCGTCAC	1500
Qy	3067	ATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCAGAGTGA	3126
Db	1501	ATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCAGAGTGA	1560
Qy	3127	CTTTTCGAAATAAATTTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAAATTTTT	3186
Db	1561	CTTTTCGAAATAAATTTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAAATTTTT	1620

Qy	3187	ACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATGTTGTTT	3246
Db	1621	ACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATGTTGTTT	1680
Qy	3247	TCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAATGTGGCCAGAAAGA	3306
Db	1681	TCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAATGTGGCCAGAAAGA	1740
Qy	3307	AAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCCACAAAC	3366
Db	1741	AAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCCACAAAC	1800
Qy	3367	TTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGTCATTTT	3426
Db	1801	TTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGTCATTTT	1860
Qy	3427	AGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCACAGTTTATTAATATATT	3486
Db	1861	AGACTCTCAATTTTAAATTAATTTTGAATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1920
Qy	3487	TAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACATCCTGA	3546
Db	1921	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTACCATGTACTGAATTTTACATCCTGA	1980
Qy	3547	TACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTTTGAAAC	3606
Db	1981	TACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTTTGAAAC	2040
Qy	3607	TACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTTTTAA	3666
Db	2041	TACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTTTTNNN	2100
Qy	3667	AAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAATTTCTTT	3726
Db	2101	NNNNNTGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAATTTCTTT	2160
Qy	3727	ACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGTTTCCTA	3786
Db	2161	ACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGTTTCCTA	2220
Qy	3787	GTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTACAGCTC	3846
Db	2221	GTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTACAGCTC	2280
Qy	3847	AAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAATGTGGAT	3906
Db	2281	AAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAATGTGGAT	2340
Qy	3907	GTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACAGTTTAT	3966
Db	2341	GTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACAGTTTAT	2400
Qy	3967	AGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGTAAAAAA	4026
Db	2401	AGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGTAAAAAA	2460

Qy 4027 TTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTTTTTTATT 4086  
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 Db 2461 TTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTTTTTTATT 2520

Qy 4087 ATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTCACTGTA 4146  
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 Db 2521 ATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTCACTGTA 2580

Qy 4147 CAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGACAAGTG 4206  
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 Db 2581 CAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGACAAGTG 2640

Qy 4207 GACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATTAAAATG 4266  
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 Db 2641 GACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATTAAAATG 2700

Qy 4267 CCACATTTCTGGTCTCTGGG 4286  
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 Db 2701 CCACATTTCTGGTCTCTGGG 2720

RESULT 11  
 AC130785/c

LOCUS AC130785 169751 bp DNA linear HTG 29-AUG-2002  
 DEFINITION Papio anubis clone RP41-325P5, WORKING DRAFT SEQUENCE.  
 ACCESSION AC130785  
 VERSION AC130785.1 GI:22218455  
 KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
 SOURCE Papio anubis (olive baboon)  
 ORGANISM Papio anubis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 Cercopithecinae; Papio.

REFERENCE 1 (bases 1 to 169751)  
 AUTHORS Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schueler,M.G., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.  
 TITLE NISC Comparative Sequencing Initiative  
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 169751)  
 AUTHORS Green,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-AUG-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA

REFERENCE 3 (bases 1 to 169751)  
 AUTHORS Green,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-AUG-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA

COMMENT ----- Genome Center

Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)

----- Project Information

Center project name: deh  
Center clone name: 325P05

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 169735 bases at least Q40  
Consensus quality: 169747 bases at least Q30  
Consensus quality: 169749 bases at least Q20  
Insert size: 138000; agarose-fp  
Insert size: 169751; sum-of-contigs  
Quality coverage: 10.99x in Q20 bases; agarose-fp  
Quality coverage: 8.94x in Q20 bases; sum-of-contigs

-----

- \* NOTE: This is a 'working draft' sequence. It currently
- \* consists of 1 contigs. Gaps between the contigs
- \* are represented as runs of N. The order of the pieces
- \* is believed to be correct as given, however the sizes
- \* of the gaps between them are based on estimates that have
- \* provided by the submitter.
- \* This sequence will be replaced
- \* by the finished sequence as soon as it is available and
- \* the accession number will be preserved.
- \* 1 169751: contig of 169751 bp in length.

FEATURES

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misc_feature	1. .63149

/note="clone overlaps with GenBank Accession Number  
AC129069 clone RP41-240D13 (center project name deg)"

BASE COUNT 51109 a 31316 c 31981 g 55345 t  
ORIGIN

Query Match 59.3%; Score 2550; DB 2; Length 169751;  
Best Local Similarity 94.8%; Pred. No. 0;  
Matches 2717; Conservative 0; Mismatches 130; Indels 19; Gaps 7;

Qy	1430	AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC	1489
Db	29218	AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC	29159
Qy	1490	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA	1549
Db	29158	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA	29099
Qy	1550	AATACAGCTCATCTTGAAAGAAGAAGCTATTTCACTGTATTTTCAATTTCTTTATATTGGACC	1609
Db	29098	AATACAGCTCATCTTGAAAGAAGAAGCTATTTCACTGTATTTTCAATTTCTTTATATTGGACC	29039
Qy	1610	GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCA	1669
Db	29038	GAAGTCATTAAAAACAAAATGAAACATTTGTCAAAAACAAAACAAAAAATATGTATTTGCA	28979
Qy	1670	CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT	1729
Db	28978	CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCATAGCTACATATGACATT	28919
Qy	1730	TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA	1789
Db	28918	TTATGAGCTGTTTACAGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCATTGTGA	28859
Qy	1790	AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT	1849
Db	28858	AAGCACTTACTTTTTTATGGTTAGCACTTCAACATAGCTCTTAATAACTCCAGGATATT	28799
Qy	1850	CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAG	1909
Db	28798	CACACAACCCTTAGGCTTAAAAATGAGCTCACTCGGAATTTCTATT-----TAAGAG	28747
Qy	1910	ATTTATTTTTTAAATCAATGGGACTCTGATATAAGGAAGAATAAGTCACGTGTAACAGAA	1969
Db	28746	ATTTATTTTTTAAATCAATGTGAATCTGATACAAAGGAAGAGTAAGTCACGTGTAACAGAA	28687
Qy	1970	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAACAACTTT	2029
Db	28686	ACTTTTAAATGAAGCTTAAATTACCCAATTTGAAATTTTAAAAATCCTTTAAAGAACTTT	28627
Qy	2030	TCAATTAATATTATCACACT-ATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTT	2088
Db	28626	TTAATTAATATTTTCACTGCTGATCAGACTGTAATTAGATGCAAATGAGAGAGTAGTT	28567
Qy	2089	TAGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAA	2148
Db	28566	TAGTTGCTGTATTTTTTGGACACTAGAAACATTTAAATGATCAGGAGGGAGTAACAGAAA	28507



Qy	2149	GAGCAAGGCTGTTTTTGAAAATCATTACA - - -CTTTCACTAGAGCCCAAACCTCAGCAT	2205
Db	28506	GAACAAGGCTGTTTTTGAAAATCATTACACTCCTTTCAGTAGAGCCCAAACCTCAGCAT	28447
Qy	2206	TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC	2265
Db	28446	TCTGCAATATGTAACCAACATGTTACAAACAAGCAGCATGTAACAACTGGCACATGTGT	28387
Qy	2266	CAGCTGAATTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGT	2325
Db	28386	CAGCCAAATCTAAATATAATACTTTTAAAAAGAAAATTATTACACCCTTTACATTTCAGA	28327
Qy	2326	TAAGATCAAACCTCACAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTT	2385
Db	28326	TAAGATCAAACCTCACAAGAGAAATAGAATGTTTGAAAGGCTGCCCCAAAGACTTCTT	28267
Qy	2386	TGAATCTGTCATTACATACCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTAT	2445
Db	28266	TGAATCTGCCATTACACAGCCTGTGAAGAAAATACTATCTACAAATTTTTTCAGGATTAT	28207
Qy	2446	TAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAAT	2505
Db	28206	TAAATCTTCTTCTTTCACTATTGTAGCTTAAACTCTGTTTGGTTTTGTCATCCGTAAAT	28147
Qy	2506	ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT	2565
Db	28146	ACTTAGCTACATACACTGCATGTAGACGATTAAACGAGGGCGGGCCCTGTGTTTCATAGTT	28087
Qy	2566	TTACGATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGT	2625
Db	28086	TTACAATGGAGAGATGCCAGTGACCTCATAATAGAGACTGTGAACTGCCTGGTGCAGTGT	28027
Qy	2626	CCACATGACAAAGGGGCAGGTAGCACCTCTCTACCCATGCTGTGGTTAAATGGTTTTC	2685
Db	28026	CCACATGACAAGGGGGCAGGTAGCACCTCTCTACCCATGCTGTAGTTAAATGGTTTTC	27967
Qy	2686	TAGCATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACA	2745
Db	27966	TAGCATATGTATAATGCTGTAGTTAAAACACTGTTTGTCAAATCATAACAGATTAGTACA	27907
Qy	2746	TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT	2805
Db	27906	TTTAATGGCTACCTGTAAAGCTTATTACTAGTTTTGTATTATTTTTGTAAATAGCCAAT	27847
Qy	2806	AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGA	2865
Db	27846	AGAAAAGTGTGCTTGACGTGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGA	27787
Qy	2866	CCGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGT	2925
Db	27786	CTGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTAAATCTTCTAAGCAAAGT	27727
Qy	2926	GCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG	2985
Db	27726	GCCTTAGAATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG	27667
Qy	2986	AGAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAA	3045

Db	27666	 AGAGGAAATGAGGTGGGGTGAGAGGAACTCATGGGGACAGATTCCCATTCTTAGCCTAA	27607
Qy	3046	CGTTCGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACAC	3105
Db	27606	 CGTTCGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACAC	27547
Qy	3106	AGTGCAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC	3165
Db	27546	 AGTGCAATGTTCTCAGAGTGACTTTAGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC	27487
Qy	3166	TTAAAATATGCCCAAATTTTTACTTTTGTCTTTTAAATAGGCTGGGCCACATGTTGGA	3225
Db	27486	 TTAAAATATGCCCAAATTTTTACTTTTTTTTCTTTTAGTAACTGGGCCACATGTTGGA	27427
Qy	3226	AATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAC	3285
Db	27426	 AATAAGCTAGTAATGTTGTTTTCTGTCAATATCGAATGTGATGGTGCAGTAAACCAAAC	27367
Qy	3286	CCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCT	3345
Db	27366	 CCAACAATGTGGCCAGAAAGAAAGAGCAATAATGATTAATTCACATGCCATGTGGATTCT	27307
Qy	3346	ATTTATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCC	3405
Db	27306	 ATTTATAAATCACCCACAACTTGTTTTTTAATTTTCATCCCAATCATTTTTTCAGAGGCC	27247
Qy	3406	TGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATT	3465
Db	27246	 TGTTATCATAGAAGACATTTTAGACTTGCAATTTTAAATTAATTTTGAATCACTAATATT	27187
Qy	3466	TTACAGTTTATTAATATA-TTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCAT	3524
Db	27186	 TTACAGTTTATTAATATATTTTTATTTCTATTTAAATTTTAGATTATTTTTATTACCAT	27127
Qy	3525	GTACTGAATTTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAA	3584
Db	27126	 GTACTGAATTTTTATATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTGTAA	27067
Qy	3585	TTATCTTGCCAAATTTTGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAA	3644
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Qy	3645	TTGCATTTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGT	3704
Db	27006	 TTGCATTTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAAATTTAACATACTGATAAGT	26948
Qy	3705	AAGAAACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTT	3764
Db	26947	 AAGAAACAATAATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATTATT	26888
Qy	3765	CAACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATT	3824
Db	26887	 TAACTTCAAACATGTTTCCTAGTATTAAGAACTTTAATATAGCAACAGACAAAATTATT	26828
Qy	3825	GTTAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTT	3884

Db 26827 GTTAACATGAATGTTACAGCTCAGAAGATTTATAAAAGATTTTAACTATTTTCTCCCTT 26768

Qy 3885 ATTATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATA 3944  
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Db 26767 ATTATCCACTGCTAATGTGGATATATGTTCAAACACCTTTTAGTATTGATAGCTTACATA 26708

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Db 26707 TGGCCAAAGGAATACAGTTTATAGTGAAACATGGGTATACTGTAGCTAACTTTATAAAAC 26648

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Db 26647 TGTAATATAACAATGTAAAAAATTATATACCTGGGGGGATTTTTTGGTTGCTTAAAGTGG 26588

Qy 4065 CTATAGTTACTGA-TTTTTTATTATGTAAGCAAAACCAATAAA---AATTTAAGTTTTT 4119  
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Db 26587 CTATAGTCACTGATTTTTTTATTATGTAAGCAAAACCAATAAACTTTAGGTTGTGTTTTT 26528

Qy 4120 TTAACAACACTACCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGT 4179  
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Db 26527 TTAACAACACTAGCTTATTTTTTCATTGTACAGGCACTAATTCATTAAATACTAATTGACTGT 26468

Qy 4180 TTAAAAGAAATATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAG 4239  
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Db 26467 TTAAAGGAAATATAAATGTGACAAGTGGACACTATTTATGTTAAATATACAATCATCAAG 26408

Qy 4240 CAAGTATGAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGG 4285  
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Db 26407 GAAGTATGAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGG 26362

# RESULT 12

AC129069/c

LOCUS AC129069 185870 bp DNA linear HTG 19-SEP-2002

DEFINITION Papio anubis clone RP41-240D13, WORKING DRAFT SEQUENCE.

ACCESSION AC129069

VERSION AC129069.2 GI:23196382

KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.

SOURCE Papio anubis (olive baboon)

ORGANISM Papio anubis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 Cercopithecinae; Papio.

REFERENCE 1 (bases 1 to 185870)

AUTHORS Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,  
 Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,  
 Cariaga,K., Coleman,B., Dietrich,N.L., Granite,S., Guan,X.,  
 Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R.,  
 Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L.,  
 Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B.,  
 Mastrian,S.D., McCloskey,J.C., McDowell,J., Paguirigan,C.,  
 Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Dugue,N.,  
 Schueler,M.G., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J.,  
 Touchman,J.W., Vogt,J.L., Walker,M., Wetherby,K.D., Wiggins,L.,  
 Young,A., Zhang,L.-H. and Green,E.D.

TITLE NISC Comparative Sequencing Initiative

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 185870)  
AUTHORS Green, E.D.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUL-2002) NIH Intramural Sequencing Center, 8717  
Grovemont Circle, Gaithersburg, MD 20877, USA  
REFERENCE 3 (bases 1 to 185870)  
AUTHORS Green, E.D.  
TITLE Direct Submission  
JOURNAL Submitted (19-SEP-2002) NIH Intramural Sequencing Center, 8717  
Grovemont Circle, Gaithersburg, MD 20877, USA  
COMMENT On Sep 19, 2002 this sequence version replaced gi:21955004.  
----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)  
----- Project Information  
Center project name: deg  
Center clone name: 240D13

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 184076 bases at least Q40  
Consensus quality: 185363 bases at least Q30  
Consensus quality: 185733 bases at least Q20  
Insert size: 152000; agarose-fp  
Insert size: 185870; sum-of-contigs  
Quality coverage: 7.20x in Q20 bases; agarose-fp  
Quality coverage: 5.89x in Q20 bases; sum-of-contigs  
-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submittor.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 185870: contig of 185870 bp in length.

FEATURES  
source Location/Qualifiers  
1. 185870  
/organism="Papio anubis"

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        /mol_type="genomic DNA"
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              clone_end:T7
              vector_side:left
              missing approximately 55 bases, including Sp6 clone end,
              on 3' end of insert"
misc_feature 121812. .185870
              /note="clone overlaps with GenBank Accession Number
              AC130785 clone RP41-325P5 (center project name deh)"
BASE COUNT   55300 a  34781 c  35402 g  60387 t
ORIGIN

Query Match          59.3%; Score 2550; DB 2; Length 185870;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 2717; Conservative 0; Mismatches 130; Indels 19; Gaps 7;

Qy      1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489
          |||
Db      151685 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC
151626

Qy      1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549
          |||
Db      151625 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA
151566

Qy      1550 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACC 1609
          |||
Db      151565 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACC
151506

Qy      1610 GAAGTCATTAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA 1669
          |||
Db      151505 GAAGTCATTAAACAAAATGAAACATTTGTCAAAAACAAAACAAAAAACTATGTATTTGCA
151446

Qy      1670 CAGCACACTATTAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATT 1729
          |||
Db      151445 CAGCACACTATTAAAATATTAAGTGTAATTATTTTAACTCATAGCTACATATGACATT
151386

Qy      1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGA 1789
          |||
Db      151385 TTATGAGCTGTTTACAGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCATTGTGA
151326

Qy      1790 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 1849
          |||
Db      151325 AAGCACTTACTTTTTTATGGTTAGCACTTCAACATAGCTCTTAATAAATCCAGGATATT
151266

Qy      1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 1909
          |||

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Db	151265	CACACAACCCTTAGGCTTAAAAATGAGCTCACTCGGAATTTCTATT-----TAAGAG	
151214			
Qy	1910	ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA	1969
Db	151213	ATTTATTTTTTAAATCAATGTGAATCTGATACAAAGGAAGAGTAAGTCACTGTAAACAGA	
151154			
Qy	1970	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAACAACTTT	2029
Db	151153	ACTTTTAAATGAAGCTTAAATTACCCAATTTGAAATTTTAAAAATCCTTTAAAGAACTTT	
151094			
Qy	2030	TCAATTAATATTATCACACT-ATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTT	2088
Db	151093	TTAATTAATATTTTCACACTGCTGATCAGACTGTAATTAGATGCAAATGAGAGAGTAGTT	
151034			
Qy	2089	TAGTTGTTGCATTTTTTCGGACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAA	2148
Db	151033	TAGTTGCTGTATTTTTTGGACACTAGAAACATTTAAATGATCAGGAGGGAGTAACTGAAA	
150974			
Qy	2149	GAGCAAGGCTGTTTTTGAAAATCATTACA---CTTTCACTAGAAGCCCAAACCTCAGCAT	2205
Db	150973	GAACAAGGCTGTTTTTGAAAATCATTACACTCCTTTCACTAGAAGCCCAAACCTCAGCAT	
150914			
Qy	2206	TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC	2265
Db	150913	TCTGCAATATGTAACCAACATGTTACAAACAAGCAGCATGTAACAAACTGGCACATGTGT	
150854			
Qy	2266	CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTCACT	2325
Db	150853	CAGCCAAATCTAAAATATAATACTTTTAAAAAGAAAAATTATTACACCTTTACATTCACT	
150794			
Qy	2326	TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTT	2385
Db	150793	TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTGCCCAAAGACTTCTT	
150734			
Qy	2386	TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTAT	2445
Db	150733	TGAATCTGCCATTACACAGCCTGTGAAGAAAAATACTATCTACAAATTTTTTTCAGGATTAT	
150674			
Qy	2446	TAAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTATCTGTAAAT	2505
Db	150673	TAAAATCTTCTTCTTTCACTATTGTAGCTTAAACTCTGTTTGGTTTTGTCTATCCGTAAAT	
150614			
Qy	2506	ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT	2565
Db	150613	ACTTAGCTACATACACTGCATGTAGACGATTAAACGAGGGCGGGCCCTGTGTTTCATAGTT	
150554			

Qy	2566	TTACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGCACTGT	2625
Db	150553	TTACAAATGGAGAGATGCCAGTGACCTCATAATAGAGACTGTGAACTGCCCTGGTGCGATGT	
	150494		
Qy	2626	CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTC	2685
Db	150493	CCACATGACAAAGGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTAGTTAAAATGGTTTC	
	150434		
Qy	2686	TAGCATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACA	2745
Db	150433	TAGCATATGTATAATGCTGTAGTTAAAACACTGTTTTGCAAATCATAACAGATTAGTACA	
	150374		
Qy	2746	TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT	2805
Db	150373	TTTAATGGCTACCTGTAAAGCTTATTACTAGTTTTTGTATTATTTTTGTAAATAGCCAAT	
	150314		
Qy	2806	AGAAAAAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAACCTGCTTTTTGAGA	2865
Db	150313	AGAAAAAGTTTGCTTGACGTGGTGCTTTTCTTTCACTTAGAGGCCAAAACCTGCTTTTTGAGA	
	150254		
Qy	2866	CCGTAAGAACCCTCTTAGCTTTGTGCGTTCTGCGCTAATTTTTATATCTTCTAAGCAAAGT	2925
Db	150253	CTGTAAGAACCCTCTTAGCTTTGTGCGTTCTGCGCTAATTTTTAAATCTTCTAAGCAAAGT	
	150194		
Qy	2926	GCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAG	2985
Db	150193	GCCTTAGAATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAG	
	150134		
Qy	2986	AGAGGAAATGAGGTGGGGTTGGAGGAAACCATGGGGACAGATTCCCATTTCTTAGCCTAA	3045
Db	150133	AGAGGAAATGAGGTGGGGTGAGAGGAAACTCATGGGGACAGATTCCCATTTCTTAGCCTAA	
	150074		
Qy	3046	CGTTCGTCATTGCCTCGTCAACATGCAAAAGGTCTGATTTTGTTCAGCAAAACAC	3105
Db	150073	CGTTCGTCATTGCCTCGTCAACATGCAAAAGGTCTGATTTTGTTCAGCAAAACAC	
	150014		
Qy	3106	AGTGCAATGTTCTCAGAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC	3165
Db	150013	AGTGCAATGTTCTCAGAGTGACTTTAGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC	
	149954		
Qy	3166	TTAAAAATATGCCCAAATTTTTACTTTTGTCTTTTAAATAGGCTGGGCCACATGTTGGA	3225
Db	149953	TTAAAAATATGCCCAAATTTTTACTTTTCTTTTAGTAACTGGGCCACATGTTGGA	
	149894		
Qy	3226	AATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAAC	3285

Db	149833		AATAAGCTAGTAATGTTGTTTTCTGTCAATATCGAATGTGATGGTGCAGTAAACCAAAC	
	149834			
Qy	3286		CCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCT	3345
Db	149833		CCAACAATGTGGCCAGAAAGAAAGAGCAATAATGATTAATTCACATGCCATGTGGATTCT	
	149774			
Qy	3346		ATTTATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCC	3405
Db	149773		ATTTATAAATCACCCACAACTTGTTTTTAATTTTCATCCCAATCATTTTTTTCAGAGGCC	
	149714			
Qy	3406		TGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATT	3465
Db	149713		TGTTATCATAGAAGACATTTTAGACTTGCAATTTTAAATTAATTTGAATCACTAATATT	
	149654			
Qy	3466		TTCACAGTTTATTAATATA-TTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCAT	3524
Db	149653		TTCACAGTTTATTAATATATTTTTATTCTATTTAAATTTTAGATTATTTTTATTACCAT	
	149594			
Qy	3525		GTACTGAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAA	3584
Db	149593		GTACTGAATTTTATATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTGTAA	
	149534			
Qy	3585		TTATCTTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAA	3644
Db	149533		TTATCTTACCAATTTTGAAACTGCACACAAAAGCATACTTGCATTATTTATAATAAAA	
	149474			
Qy	3645		TTGCATTTCAGTGGCTTTTTAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT	3704
Db	149473		TTGCATTTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT	
	149415			
Qy	3705		AAGAAACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTT	3764
Db	149414		AAGAAACAATAATAATTTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATTATT	
	149355			
Qy	3765		CAACTTCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATT	3824
Db	149354		TAACTTCAAAACATGTTTCCTAGTATTAAGAACTTTAATATAGCAACAGACAAAATTATT	
	149295			
Qy	3825		GTTAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTT	3884
Db	149294		GTTAACATGAATGTTACAGCTCAGAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTT	
	149235			
Qy	3885		ATTATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATA	3944



Db 149234 ATTATCCACTGCTAATGTGGATATATGTTCAAACACCTTTTAGTATTGATAGCTTACATA  
149175

Qy 3945 TGGCCAAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAG 4004  
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Db 149174 TGGCCAAAGGAATACAGTTTATAGTGAAACATGGGTATACTGTAGCTAACTTTATAAAAC  
149115

Qy 4005 TGTAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGG 4064  
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Db 149114 TGTAATATAACAATGTAAAAAATTATATACCTGGGGGGATTTTTTGGTTGCTTAAAGTGG  
149055

Qy 4065 CTATAGTTACTGA-TTTTTTATTATGTAAGCAAAACCAATAAA----AATTTAAGTTTTT 4119  
|||||

Db 149054 CTATAGTCACTGATTTTTTTATTATGTAAGCAAAACCAATAAACTTTAGGTTGTGTTTTT  
148995

Qy 4120 TTAACAACTACCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGT 4179  
|||||

Db 148994 TTAACAACTAGCTTATTTTTTCATTGTACAGGCACTAATTCATTAAATACTAATTGACTGT  
148935

Qy 4180 TTAAAAGAAATATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAG 4239  
|||||

Db 148934 TTAAAGGAAATATAAATGTGACAAGTGGACACTATTTATGTTAAATATACAATCATCAAG  
148875

Qy 4240 CAAGTATGAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGG 4285  
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Db 148874 GAAGTATGAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGG 148829

# RESULT 13

AR165435

LOCUS AR165435 1873 bp DNA linear PAT 17-OCT-2001

DEFINITION Sequence 13 from patent US 6280931.

ACCESSION AR165435

VERSION AR165435.1 GI:16240327

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Sakamoto,A. and Hanaoka,F.

TITLE Method for specifically amplifying a dystroglycan,  
.alpha.-sarcoglycan, or endothelin Breceptor cDNA of an extremely  
small

JOURNAL Patent: US 6280931-A 13 28-AUG-2001;

FEATURES Location/Qualifiers

source 1. 1873

/organism="unknown"

BASE COUNT 490 a 434 c 438 g 511 t

ORIGIN

Query Match 39.3%; Score 1691.8; DB 6; Length 1873;  
Best Local Similarity 99.6%; Pred. No. 6.1e-293;

Matches 1696; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy	178	TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC	237
Db	171	TGTCCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC	230
Qy	238	ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGC	297
Db	231	ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGC	290
Qy	298	CTGTCGCGGATCTGGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG	357
Db	291	CTGTCGCGGATCTGGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG	350
Qy	358	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	417
Db	351	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	410
Qy	418	AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	477
Db	411	AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	470
Qy	478	CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	537
Db	471	CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	530
Qy	538	AAATACATCAACACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCC	597
Db	531	AAATACATCAACACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCC	590
Qy	598	ACACTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATC	657
Db	591	ACACTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATC	650
Qy	658	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	717
Db	651	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	710
Qy	718	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA	777
Db	711	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	CGAGCTGTTGCTTCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	957
Db	891	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010

Qy	1018	CAGAAGACAGCTTTTCATGCAAGTTTACAAAGACAGCAAAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	1011	CAGAAGACAGCTTTTCATGCAAGTTTACAAAGACAGCAAAAAGATTGGTGGCTATTTCAGTTTC	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCCTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCCTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
Db	1251	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1310
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGTC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGTC	1370
Qy	1378	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1437
Db	1371	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1430
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGC	1497
Db	1431	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGC	1490
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGC	1557
Db	1491	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGC	1550
Qy	1558	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT	1617
Db	1551	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT	1610
Qy	1618	TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1677
Db	1611	TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1670
Qy	1678	TATTAATAATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1737
Db	1671	TATTAATAATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1730
Qy	1738	TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1797
Db	1731	TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1790
Qy	1798	AATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTACACAAC	1857
Db	1791	AATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTACACAAC	1850

Qy 1858 ACTTAGGCTTAAAAATGAGCTCA 1880  
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 Db 1851 ACTTAGGCTTAAAAATGAGCTCA 1873

RESULT 14

E15242

LOCUS E15242 1873 bp DNA linear PAT 28-JUL-1999

DEFINITION Human mRNA for endothelin B receptor, complete cds.

ACCESSION E15242

VERSION E15242.1 GI:5709925

KEYWORDS JP 1998057064-A/13.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Sakamoto, E. and Hanaoka, F.

TITLE SPECIFIC AMPLIFICATION OF MINOR GENE PRODUCT

JOURNAL Patent: JP 1998057064-A 13 03-MAR-1998;

RIKAGAKU KENKYUSHO

COMMENT OS Homo sapiens (human)

PN JP 1998057064-A/13

PD 03-MAR-1998

PF 16-AUG-1996 JP 1996216506

PI SAKAMOTO EIJI, HANAOKA FUMIO

PC C12N15/09, C07H21/02, C07H21/04//C12Q1/68;

CC strandedness: Double;

CC topology: Linear;

FH Key Location/Qualifiers

FH

FT source 1. .1873

FT /organism='Homo sapiens'

FT /tissue\_type='peripheral blood' FT CDS

231. .1559

FT /product='endothelin B receptor'.

FEATURES Location/Qualifiers

source 1. .1873

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

BASE COUNT 490 a 434 c 438 g 511 t

ORIGIN

Query Match 39.3%; Score 1691.8; DB 6; Length 1873;

Best Local Similarity 99.6%; Pred. No. 6.1e-293;

Matches 1696; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237

|| || |||||

Db 171 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 230

Qy 238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297

|||||

Db 231 ATGCAGCCGCCTCCAAGTCTGTGCGGACCGGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 290

Qy 298 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357

Db	291	 CTGTGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG	350
Qy	358	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	417
Db	351	 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	410
Qy	418	AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	477
Db	411	 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	470
Qy	478	CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	537
Db	471	 CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	530
Qy	538	AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTC	597
Db	531	 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTC	590
Qy	598	ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC	657
Db	591	 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC	650
Qy	658	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	717
Db	651	 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	710
Qy	718	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA	777
Db	711	 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	957
Db	891	 GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	 GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	1011	 CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTATTTCAGTTTC	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	 TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197

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Db	1731	TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1790
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RESULT 15

S44866

LOCUS	S44866	1872 bp	mRNA	linear	PRI 07-MAY-1993
DEFINITION	ETB endothelin receptor [human, mRNA, 1872 nt].				
ACCESSION	S44866				
VERSION	S44866.1 GI:233233				

KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1872)  
 AUTHORS Sakamoto,A., Yanagisawa,M., Sakurai,T., Takuwa,Y., Yanagisawa,H.  
 and Masaki,T.  
 TITLE Cloning and functional expression of human cDNA for the ETB  
 endothelin receptor  
 JOURNAL Biochem. Biophys. Res. Commun. 178 (2), 656-663 (1991)  
 MEDLINE 91315496  
 PUBMED 1713452  
 REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI gibbsq 44866] from the original journal article.  
 This sequence comes from Fig. 1.  
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 INTVVSCLVFVLGIIGNSTLLRI I Y K N K C M R N G P N I L I A S L A L G D L L H I V I D I P I N V Y  
 K L L A E D W P F G A E M C K L V P F I Q K A S V G I T V L S L C A L S I D R Y R A V A S W S R I K G I G V P K W T  
 A V E I V L I W V V S V L A V P E A I G F D I I T M D Y K G S Y L R I C L L H P V Q K T A F M Q F Y K T A K D W W  
 L F S F Y F C L P L A I T A F F Y T L M T C E M L R K K S G M Q I A L N D H L K Q R R E V A K T V F C L V L V F A L  
 C W L P L H L S R I L K L T L Y N Q N D P N R C E L L S F L L V L D Y I G I N M A S L N S C I N P I A L Y L V S K R  
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 BASE COUNT 489 a 434 c 438 g 511 t  
 ORIGIN  
 Query Match 39.3%; Score 1690.8; DB 9; Length 1872;  
 Best Local Similarity 99.6%; Pred. No. 9.3e-293;  
 Matches 1695; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 Qy 178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237  
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Db	1011	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTATTTCAGTTTT	1070
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Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
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Db	1191	 GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
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Db	1251	 CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1310
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
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 Job time : 15106.3 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:17:01 ; Search time 7748.55 Seconds  
(without alignments)  
13490.718 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: em\_estba:\*  
2: em\_esthum:\*  
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4: em\_estmu:\*  
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6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
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20: em\_gss\_vrt:\*  
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22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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			Match	Length				
		Score	%					
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	2	1371.2	31.9	3990	11	AK085532		AK085532 Mus muscu
	3	1137.6	26.4	2521	11	AK082103		AK082103 Mus muscu
	4	1126.4	26.2	3611	11	AK085165		AK085165 Mus muscu
	5	1020	23.7	2669	11	AK076426		AK076426 Mus muscu
c	6	987	22.9	1201	9	AL571798		AL571798 AL571798
c	7	866	20.1	957	12	BI520706		BI520706 603071813
c	8	860.2	20.0	1201	9	AL553041		AL553041 AL553041
	9	851	19.8	942	9	AL543805		AL543805 AL543805
	10	848	19.7	891	13	BQ229233		BQ229233 AGENCOURT
	11	816.2	19.0	1201	9	AL546465		AL546465 AL546465
	12	808.6	18.8	972	12	BI858627		BI858627 603389094
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	14	794.8	18.5	884	13	BU557315		BU557315 AGENCOURT
	15	792	18.4	911	13	BQ719386		BQ719386 AGENCOURT
c	16	788	18.3	1201	9	AL571072		AL571072 AL571072
	17	773.6	18.0	852	13	BU172663		BU172663 AGENCOURT
	18	772	17.9	1201	9	AL553065		AL553065 AL553065
c	19	766.6	17.8	775	14	CA771707		CA771707 io81f04.x
	20	741.8	17.2	770	12	BM014035		BM014035 603639686
c	21	740.2	17.2	942	13	BX345882		BX345882 BX345882
	22	738	17.2	999	13	BX417121		BX417121 BX417121
	23	736	17.1	1201	9	AL545283		AL545283 AL545283
	24	734.2	17.1	978	13	BQ683643		BQ683643 AGENCOURT
	25	732.8	17.0	1121	12	BM926545		BM926545 AGENCOURT
	26	729.2	17.0	758	12	BM014042		BM014042 603639695
	27	727.8	16.9	885	12	BG769122		BG769122 602743382
	28	718	16.7	785	9	AU117045		AU117045 AU117045
	29	712.8	16.6	743	9	AU138228		AU138228 AU138228
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c	31	706.2	16.4	800	9	AI760041		AI760041 wg57e06.x
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c	33	703	16.3	722	12	BM970305		BM970305 UI-CF-EC1
c	34	698.8	16.2	726	9	AI422064		AI422064 tf57c12.x
c	35	697.4	16.2	866	9	AI188458		AI188458 qd14d01.x
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c	40	673	15.6	699	12	BM974913		BM974913 UI-CF-EC1
c	41	662.6	15.4	751	9	AA651686		AA651686 nm47b02.r
	42	661.6	15.4	941	13	BX345883		BX345883 BX345883
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## ALIGNMENTS

## RESULT 1

AK083415

LOCUS AK083415 3878 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030003K13 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK083415

VERSION AK083415.1 GI:26350536

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

## REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409 (6821), 685-690 (2001)  
MEDLINE 21085660  
PUBMED 11217851  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE 6 (bases 1 to 3878)  
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission  
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers  
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Qy	850	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
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Qy	910	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
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Qy	970	ATGGACTIONCAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAAGACAGCT	1029
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Qy	1030	TCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTG	1089
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Qy	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAA	1149
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Qy	1150	AGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACC	1209
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Qy	1210	GTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATT	1269
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Qy	1270	CTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTG	1329
Db	1141	CTGAAGCTCACCTGTATGACCAGAGCAATCCACACAGGTGTGAGCTTCTGAGCTTTTTG	1200
Qy	1330	TTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATT	1389
Db	1201	TTGGTTTTGGACTACATTGGTATCAACATGGCTTCTTTGAACTCCTGCATCAATCCAATC	1260
Qy	1390	GCTCTGTATTTGGTGAGCAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGG	1449
Db	1261	GCTCTGTATTTGGTGAGCAAAGATTCAAAAAGTCTTTAAGTCATGTTTGTGCTGCTGG	1320
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Db	1321	TGCCAAACGTTTGGAGGAAAAGCAGTCCTTGAGGAGAAGCAGTCCTGCCTGAAGTTCAAA	1380
Qy	1510	GCTAATGATCACGGATATGACAACCTCCGTTCAGTAATAAATACAGCTCATCTTGAAAG	1569
Db	1381	GCCAACGATCACGGATATGACAACCTCCGTCCAGCAATAAATACAGCTCGTCTTGAAGG	1440
Qy	1570	AAGAACTATTCACTGTATTTTCATTTTTCTTTATATTGGACC GAAGTCATTAAAA CAAAAATG	1629
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Qy	1630	AAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTATTAAAA TATT	1689
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Qy	1690	AAGTGTAATTATTTTAACTCTACAGCTACATATGAC-----ATTTTATGAGCTGTTTAC	1744
Db	1561	AGAGGGATTATTTTAACTGTTCTGACGCTCAACACCGGATATATTCACGGGCTGTTTAC	1620
Qy	1745	GGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAATTTTTT	1804
Db	1621	AACCTAAGAAAGCTGTGGGAAGGAATGAAGCCCTCCTCCGTGGGGAAGCACTTAGATTCT	1680
Qy	1805	TACAGTTAGCACTTCAACATAGCTCTTAACTTCCAGGATATTCACACAACACTTAGG	1864
Db	1681	T--AGTCAGCACTTCAGCAGAGCTCTTAAAGCCCCCTAGTGCGTTTACATGCCACTTACG	1738
Qy	1865	CTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTAAATC	1924
Db	1739	TTTAAAAA-----AACGAGAACTTCACTGAAGTTCTGTTTCAGGAGTTTATTATCCAGT	1791
Qy	1925	AATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAA CAGAACTTTTAAATGAAGC	1984
Db	1792	CCTATGAATCTGGATTCAAGAAAGCAT--GACATTGCAAAACAATTCTTAAACGAAGTT	1849
Qy	1985	TTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAA CAACCTTTTCAATTAATATTATC	2044
Db	1850	TCAATTGCTTAATTTGAACTTAAAAAAAAAAAAAAAACTAATAAATTTTTATGCATACTATC	1909
Qy	2045	--ACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCA-TT	2101
Db	1910	ATACCCACTAATCTGATTGTAAGTATATGCAAAAGAAAAGGCAATATGGTTGCTAAACTT	1969
Qy	2102	TTTCGGACACTGGAAA CATTTAAATGATCAGGAGGGAGTAACAGAAAAGAGCAAGGCTGTT	2161
Db	1970	TTTTGGTCATTACCAACATTGAAATGATCAGAATTCGGGGGAAGAAA-----	2016
Qy	2162	TTTGAAAA TCATTACACTTTCACTAGAAAGCCCAAACCTCAGCATTTCTGCAATATGTAACC	2221
Db	2017	-----AGACAGCC	2024
Qy	2222	AACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAAAT	2281
Db	2025	TGCGAATGCCACAGAGAAAACATGGGAAAGCGTG-----	2058
Qy	2282	ATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCAC	2341
Db	2059	-----AGCTGCTATGCCTGAGACTTCTGAAATTCCTCACACATACTCTGCAG	2106



Qy 2342 AAAGAGAAATAGAATGTTTGAAGGCTATCCCAAAGACTTTTTGAATCTGTCATTAC 2401  
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 Db 2107 AAAGACACAAA-----ACAGAACTACCTATGATTTCTTTAAAGTTCTTTCAAAT 2157

Qy 2402 ATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTTTT 2461  
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Qy 2462 CACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTATCTGTAAATACTTACCTACATACAC 2521  
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 Db 2204 -----TCTGTAAATACTTAGCTATTAGCTATAAGCAC 2235

Qy 2522 TGCATGTAGATGATTAAATGA--GGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGA 2579  
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 Db 2236 TACACGTAGAGGACTTAAACAAAGGCAGGTCCCAGCGTTCGTAGCTTTCTGACAAAGAGA 2295

Qy 2580 TGCCAGTGACCTCATAAT--AAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAA 2637  
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 Db 2296 TGCCAGTAACCCGGTTATAGACAGAATGTGAATTGCCCGGTGCAGTGTCCACATGGCAAA 2355

Qy 2638 GGGGCAGGTAGCACCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTAT 2697  
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 Db 2356 GAAGCAGGGAGCATC--CTTTCAGCCATGCTGTAGAGAAAATGGTCCACAGC-----AC 2407

Qy 2698 AATGCTATAGTTAAAATACTATTTTTCAAATCATAAGATTAGT-ACATTTAACAGCTA 2756  
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Qy 2876 CTCTTAGCTTTGTGCGTTCCCTGCCTAATTTTTATATCTTCTAAGCAAA----- 2923  
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Qy 2924 --GTGCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGA 2981  
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Qy 2982 AGAGAGAGGAAATGAGGTGGGGTTGGAGGAAACCATGGGGACAGATTCCCATTCTTAGC 3041  
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Qy 3042 CTAACGTTTCGTCAATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAA 3101  
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 Db 2826 ACAAAGCGCAGCGTTCTCAGCGTGAC-TCGGGAACAAACCAAGCCCGAGAGCTTTAACCT 2884

Qy	3162	GGTCTTAAAAATATGCCCAAATTTT-----	3185
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Db	3005	TTGAAATGAGCTTAAACAATGCAGTTTCTACCAAATCATGTGTGACAATACAATAAACC	3064
Qy	3281	AAAACCCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGG	3340
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Qy	3401	AGGCCTGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAAATT-TTGAATCACT	3459
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Qy	3520	ACCATGTACTGAATTTTTTACATCCTGATACCCCTTTCCTTCTCCATGT-----CAGTA	3571
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Qy	3632	ATTTATAATAAAATTGCATTTCAGTGGCTTTTTAAAAAAAATGTTTGATTCAAAACTTTAA	3691
Db	3401	ATATACAATAAACTATATTAAGTGGCTTTTTTATTAAAAATTTTAGCACA-----CAG	3454
Qy	3692	CATACTGATAAGTAAGAAACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAA	3751
Db	3455	ACCAAGGGTGATAAGAAAAAAAACATGATTCCCTTGATAATTAAAAACCAAGATAAGAGA	3514
Qy	3752	AGGTGCTATCGTTCAACTTCAAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAAC	3811
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Qy	3812	AGACAAAAATTATTGTTAACATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACC	3871
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Qy	3872	TATTTTCTCCCTTATTATCCACTGCTAATGTGGATGTATGTTCAACACCTTTTAGTATT	3931
Db	3632	TATTTTCTCCCAAATTAATTAAGTCTATTTTGGTCTGTGTTCAAACA-TTTTCAGTATT	3690
Qy	3932	GATAGCTTACATATGGCCAAAGGAATACAGTTTATAGCAAAAACATGGGTATGCTGTAGCT	3991

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Db      3691 GATAATGTGCA-ACAGCCAAAGGAACACTGTTTTTCATCCAAATGCGGGTGTGTTGTACCT 3749

Qy      3992 AACTTTATAAAAGTGTAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTTGG 4051
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Db      3750 AAC---ATGCACTTGTAATAAAGCCGTGTAAAA---TAACTGTGTTTTGTTTTGCTCTGG 3803

Qy      4052 TTGCCTAAAGTGGC-----TATAGTTACTGATTTTTTTATTATGTAAGCAAAACCAATAA 4105
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Qy      4106 AAATTTAAGTTTTTTT 4120
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## RESULT 2

AK085532

LOCUS AK085532 3990 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630038G12 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK085532

VERSION AK085532.1 GI:26351656

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

## REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3990)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/

URL: <http://fantom.gsc.riken.go.jp/>.

FEATURES

source 1. 3990

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/strain="C57BL/6J"

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ORIGIN

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Best Local Similarity 66.0%; Pred. No. 3.2e-184;

Matches 2664; Conservative 0; Mismatches 1043; Indels 327; Gaps 34;

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Db 237 AGCCGGTGCGGACGCGCCTTGGTGGCGCTGCTGCTGGCCTGTGGCTTCTTGGGGGTATGG 296

Qy 313 GGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTC---CGCTTTTGCAAACCGCAGAG 369

Db 297 GGAGAGAAAAGAGGATTCCACCTGCCCAAGCCACGCTGTCACTTCTCGGGACTAAAGAG 356

Qy 370 ATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGG 429

Db 357 GTAATGACGCCACCCACTAAGACCTCCTGGACCAGAGGTTCCAACCTCCAGTCTGATGCGT 416

Qy 430 TCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACC 489

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Db	476	--CTTCCCTCCTCCGTGCCAACGAAATATTGAGATCAGCAAGACTTTTAAATACATCAAC	533
Qy	550	ACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGA	609
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Qy	610	ATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCT	669
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Qy	670	CTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCA	729
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Qy	910	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
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Qy	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT	1029
Db	954	TCGGACTACAAAGGAAAGCCCCTAAGGGTCTGCATGCTTAATCCCTTTCAGAAAACAGCC	1013
Qy	1030	TTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTG	1089
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Qy	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAA	1149
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Qy	1150	AGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACC	1209
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Qy	1210	GTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGGATT	1269
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Qy	1330	TTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATT	1389
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Qy	1450	TGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAA	1509
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Db	1554	CAAGAACACTCGCCGAATCTCACTGTCTCATTTGTGGACAGATACCATTAAAACAAAATG	1613
Qy	1630	AAACATTTGCCAAAAACAAAACAAAAAATATGTATTTGCACAGCACACTATTAAAAATATT	1689
Db	1614	AAACCGTTGCCAAATCAAATGGAAAAAACCATGTAGCAGAAAGGTGTGCGCGCGTGTG	1673
Qy	1690	AAGTGTAATTATTTTAACTCAGCTACATATGAC-----ATTTTATGAGCTGTTTAC	1744
Db	1674	AGAGGGATTATTTTAACTGTTCTGACGCTCAACACCGGATATATTCACGGGCTGTTTAC	1733
Qy	1745	GGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCTGAAAGCACTTAATTTTT	1804
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Qy	1805	TACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCAACAACACTTAGG	1864
Db	1794	T--AGTCAGCACTTCAGCAGAGCTCTTAAAGCCCCTAGTGCGTTACATGCCACTTACG	1851
Qy	1865	CTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAATC	1924
Db	1852	TTTAAAAA-----AACGAGAACTTCACTGAAGTTCTGTTCAGGAGTTTATTATCCAGT	1904
Qy	1925	AATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATGAAGC	1984
Db	1905	CCTATGAATCTGGATTCAAGAAAGCAT--GACATTGCAAAACAATTCTTAAACGAAGTT	1962
Qy	1985	TTAAATTACTCAATTTAAATTTTAAATCCTTTAAAACAACTTTTCAATTAATATTATC	2044
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Qy	2045	--ACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCA--TT	2101
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Qy 2342 AAAGAGAAATAGAATGTTTGAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTAC 2401  
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Qy 2402 ATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAATCTTCTTTTTT 2461  
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Qy	3162	GGTCTTAAATATGCCCAAATTTT-----	3185
Db	2998	 TGTCTTAAATATAACAGATTTTCTTCCTTCCTTTTCTCTTTCTTCTCTTCTCTCTC	3057
Qy	3186	-----TACTTTGTTTTTCTTTTAAATAGGCTGGGCCACATG	3220
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Qy	3632	ATTTATAATAAAATTCGATTTCAGTGGCTTTTTTAAAAAAATGTTTGATTCAAACTTTTAA	3691
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Qy	3752	AGGTGCTATCGTTCAACTTCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAAC	3811



Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2521)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),



Qy 370 ATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGG 429  
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 Db 348 GTAATGACGCCACCCACTAAGACCTCCTGGACCAGAGGTTCCAACCTCAGTCTGATGCGT 407

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#### RESULT 4

AK085165

LOCUS AK085165 3611 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430047G06 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK085165

VERSION AK085165.1 GI:26351484

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

#### REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

#### REFERENCE

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AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

#### REFERENCE

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AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,

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 Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.  
 and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409 (6821), 685-690 (2001)  
 MEDLINE 21085660  
 PUBMED 11217851  
 REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3611)  
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
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 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
 Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.go.jp/  
 URL:http://fantom.gsc.riken.go.jp/.

FEATURES  
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 Qy 3307 AAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCCACAAAC 3366  
 Db 3235 AAGAACAATACTGAATCCACGTGACAC----ATGACTCTCTTTAGGAGTCACCCACAGTT 3290  
 Qy 3367 TTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGTCATTTT 3426  
 Db 3291 CTTGTGTGTA-----CAGATTGCTTTTTAATCATAAAGGACGCCCC 3331  
 Qy 3427 AGACTCTCAATTTTAAATTAATT-TTGAATCACTAATATTTTCACAGTTTATTAATATAT 3485  
 Db 3332 AGATCTTCAATTTTAAAGTTAGTTATTGGCTCCCCAGTAGTTTCACAGCGTGGATATATTT 3391  
 Qy 3486 TTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACATCCTG 3545  
 Db 3392 TTAATTTTACT-AAGTTTTAGATTGGTTTTATTGTTGTGTTCTAAATCTTAAGTCCTA 3450  
 Qy 3546 ATACCCTTTCCT-----TCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAA 3597  
 Db 3451 ACATCTTTGTTTAAACCCAGATGTTCCCTTCCCTCTTCATGGGCAATAATCGTCCCTGCCAAA 3510  
 Qy 3598 TTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGG 3657  
 Db 3511 TTATGAAATGGCATAAGAATACTATTACATAATATATACAATAAACTATATTAAGTGG 3570  
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 Db 3571 CTTTTTTTATTAAAAATTTTA 3591

# RESULT 5

AK076426

LOCUS AK076426 2669 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832401B07 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK076426

VERSION AK076426.1 GI:26345371

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,  
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
 Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,  
 Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,  
 Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,  
 Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,  
 Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,  
 Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,  
 Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,  
 Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,  
 Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,  
 Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,  
 Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,  
 Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,  
 Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,  
 Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,  
 Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,  
 Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,  
 Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,  
 Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.  
 and Hayashizaki,Y.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409 (6821), 685-690 (2001)  
 MEDLINE 21085660  
 PUBMED 11217851  
 REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 2669)  
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,

Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .2669 /organism="Mus musculus" /mol\_type="mRNA" /strain="C57BL/6J" /db\_xref="FANTOM\_DB:4832401B07" /db\_xref="taxon:10090" /clone="4832401B07" /tissue\_type="head" /clone\_lib="RIKEN full-length enriched mouse cDNA library" /dev\_stage="0 day neonate"

CDS 220. .1548 /note="unnamed protein product; ENDOTHELIN B RECEPTOR PRECURSOR (SWISSPROT|P48302, evidence: FASTY, 100%ID, 100%length, match=1326) putative" /codon\_start=1 /protein\_id="BAC36337.1" /db\_xref="GI:26345372" /translation="MQSPASRCGRALVALLACGFLGVWGEKRGFPAPAQATLSLLGTK EVMTPTTKTSWTRGSNSSLMRSSAPAEVTKGGRGAGVPPRSFPPPCQRNIEISKTFKY INTIVSCLVFLGIIGNSTLLRIIYKNKCMRNGPNILIASLALGDLHLIIIDIPINTY KLLAEDWPFGAEMCKLVPFIQKASVGITVLSLCALSIDRYAVASWSRIKGIGVPKWT AVEIVLIWVSVVLAVPEAIGFDMITS DYK GKPLRVCM LNPFQKTA FMQFYKTAKDWW LFSFYFCLPLAITAVFYTLMTCEMLRKKSGMQIALNDHLKQRREVAKTVFCLVLVFAL CWLPLHLSRI LKLTLYDQSNPHRC ELLSFLLVLDYIGINMASLNSCINPIALYLVSKR FKNCFKSC LCCWCQT FEEKQSLEEKQSCLKFKANDHGYDNFRSSSNKYSSS"

BASE COUNT 714 a 613 c 593 g 749 t

ORIGIN

Query Match 23.7%; Score 1020; DB 11; Length 2669;  
 Best Local Similarity 84.7%; Pred. No. 1.4e-134;  
 Matches 1169; Conservative 0; Mismatches 205; Indels 6; Gaps 2;

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Db	175	AAACAGCAGAGCGGCTACCAGACTCTCACAGGAGCAAGCTGTAACATGCAATCGCCCCGA	234
Qy	253	AGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTGTGCGGATCTGG	312
Db	235	AGCCGGTGTGCGGACGCGCCTTGGTGGCGCTGCTGCTGGCCTGTGGCTTCTTGGGGGTATGG	294
Qy	313	GGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTC---CGCTTTTGCAAACCGCAGAG	369
Db	295	GGAGAGAAAAGAGGATTCCCACTGCCCAAGCCACGCTGTCACTTCTCGGGACTAAAGAG	354
Qy	370	ATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGG	429
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Qy	490	ATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAAC	549
Db	474	--CTTCCCTCCTCCGTGCCAACGAAATATTGAGATCAGCAAGACTTTTAAATACATCAAC	531
Qy	550	ACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACTCCACACTTCTGAGA	609
Db	532	ACGATTGTGTCTGTGCCTCGTGTTCTGTGCTAGGCATCATCGGGAACTCCACGCTGCTAAGA	591
Qy	610	ATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCT	669
Db	592	ATCATCTACAAGAACAAAGTGCATGCGCAATGGTCCCAATATCTTGATCGCCAGTCTGGCT	651
Qy	670	CTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCA	729
Db	652	CTGGGAGACCTACTGCACATCATCATAGACATACCCATTAAACACCTACAAGTTGCTCGCA	711
Qy	730	GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	789
Db	712	GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAGGCTTCT	771
Qy	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Db	772	GTGGGAATCACAGTGCTGAGTCTTTGTGCTCTAAGTATTGACAGATATCGAGCTGTTGCT	831
Qy	850	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Db	832	TCTTGGAGTCGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTTA	891
Qy	910	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Db	892	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCGAAGCCATAGGTTTTGATATGATTACG	951
Qy	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT	1029







Db	713	TTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTT	654
Qy	909	GATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTAC	968
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Qy	969	GATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGC	1028
Db	593	GATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGC	534
Qy	1029	TTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTT	1088
Db	533	TTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTT	474
Qy	1089	GCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAA	1148
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Db	293	TCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCT	234
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Qy	1389	TGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTG	1448
Db	173	TGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTG	114
Qy	1449	GTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAA	1508
Db	113	GTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAA	54
Qy	1509	AGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCAT	1561
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# RESULT 7

BI520706/c

LOCUS	BI520706	957 bp	mRNA	linear	EST 29-AUG-2001
DEFINITION	603071813T1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163746 3', mRNA sequence.				
ACCESSION	BI520706				
VERSION	BI520706.1 GI:15345498				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				



Db 777 CTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGA 718

Qy 809 GTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAG 868  
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Db 717 GTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAG 658

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Qy 929 TTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAGGAAGTT 988  
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Db 597 TTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAGGAAGTT 538

Qy 989 ATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTTCATGCAGTTTTACAAGA 1048  
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Qy 1049 CAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCAT 1108  
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Db 477 CAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCAT 418

Qy 1109 TT-TTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCT 1167  
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Db 417 TTGTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCT 358

Qy 1168 TTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTT 1227  
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Db 357 TTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTT 298

Qy 1228 GTCTTTGCCCTCTGCTGGCTTCCCTTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTAT 1287  
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Qy 1348 GGTATCAACATGGCTTCACTGAATTCTGCATTAACCCAATTGCTCTGTATTTGGTGAGC 1407  
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Db 177 GGTATCAACATGGCTTCACTGAATTCTGCATTAACCCAATTGCTCTGTATTTGGTGAGC 118

Qy 1408 AAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCT-GCTGGTGCCAGTCATTTGAAGA 1466  
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Db 117 AAAAGATTCAACAAGTCTTTAAGTCATGCTTATGCTGGCTGGTGCCAGTCATTTGAAGA 58

Qy 1467 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATG 1516  
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RESULT 8

AL553041/c

LOCUS AL553041 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL553041 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI072YK22 3-PRIME, mRNA sequence.

ACCESSION AL553041

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VERSION      AL553041.2   GI:31274855
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 1201)
AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished
COMMENT       On Feb 15, 2001 this sequence version replaced gi:12892503.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. This sequence belongs to sequence cluster 7006.r For
              more information about this cluster, see
              http://www.genoscope.cns.fr/
              cgi-bin/cluster.cgi?seq=CS0DI072BF11NP1&cluster=7006.r. Contact :
              Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
              Faraday Avenue Genoscope sequence ID : CS0DI072BF11NP1.

FEATURES             Location/Qualifiers
     source            1. .1201
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                       /note="1st strand cDNA was primed with a NotI-oligo(dT)
                       primer. Five prime end enriched, double-strand cDNA was
                       digested with Not I and cloned into the Not I and EcoR V
                       sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT      428 a      102 c      202 g      394 t      75 others
ORIGIN

Query Match      20.0%; Score 860.2; DB 9; Length 1201;
Best Local Similarity 89.9%; Pred. No. 6.2e-112;
Matches 966; Conservative 32; Mismatches 54; Indels 22; Gaps 7;

Qy      3179 AAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAA 3238
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Db      1061 AAATCCMAAATTAMCTTTTTTYTTTAAWGWKCKGKCCACWKTKKRAAAK-----CTWKA 1007

Qy      3239 TGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGC 3298
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Db      1006 AATTTKTTTCTTCCAATATTAATTTT-----TTTACATAAACCAAACCAACAATTTKCC 952

Qy      3299 CAGAAAGAAAGAGCAATAATAATTAATTCACACCATATGGATTCTATTTATAAATCAC 3358
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Db      951 ATAAAKTAA--KKTCAWTATWATTAATTCACMCMCCATATKTATYCTATTTATAAATCAC 894

Qy      3359 CCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTATCATAGAA 3418
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Db      893 CCACAWACTTKTTCTTTAATTCMWTCCCAATCACTTTTTTCAGAGKCTGTATCATAGAA 834

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Qy 3419 GTCATTTTAGACTCTCAATTTTAAATT-AATTTTGAATCACTAATATTTTCACAGTTTAT 3477  
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Qy 3478 TAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTT 3537  
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 Db 414 TTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCT 355

Qy 3898 AATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAAT 3957  
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Qy 3958 ACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAA 4017  
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 Db 294 ACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAA 235

Qy 4018 TGTAATAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGA 4077  
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 Db 234 TGTAATAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGA 175

Qy 4078 TTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTT-AACAACTACCTTATT 4136  
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 Db 174 TTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTCAACAACTACCTTATT 115

Qy 4137 TTTCACTGTACAGACACTAATTCATTAAATACTAA-----TTGATTGTTTAAAAGAAA 4189  
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 Db 114 TTTCACTGTACAGACACTAATTCATTAAATACTCACACTCTCGCACTTGTTTAAAAGAAA 55

Qy 4190 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAG 4243  
 ||| : |||  
 Db 54 TATAAAKGBGMCAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAG 1







```

5', mRNA sequence.
ACCESSION   BQ229233
VERSION     BQ229233.1  GI:20410633
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 891)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: ATCC/DCTD/DTP
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM13315 row: e column: 17
              High quality sequence stop: 696.

FEATURES             Location/Qualifiers
     source            1..891
                       /organism="Homo sapiens"
                       /mol_type="mRNA"
                       /db_xref="taxon:9606"
                       /clone="IMAGE:6055288"
                       /tissue_type="melanotic melanoma"
                       /lab_host="DH10B (phage-resistant)"
                       /clone_lib="NIH_MGC_72"
                       /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                       Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                       Average insert size 2 kb. Library constructed by Life
                       Technologies."

BASE COUNT      291 a      162 c      155 g      283 t
ORIGIN

Query Match      19.7%; Score 848; DB 13; Length 891;
Best Local Similarity 99.1%; Pred. No. 3.6e-110;
Matches 884; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

Qy      2086 GTTTAGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAG 2145
          |||
Db      1 GTTTAGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAG 60

Qy      2146 AAAGAGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCAT 2205
          |||
Db      61 AAAGAGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCAT 120

Qy      2206 TCTGCAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGTC 2265
          |||
Db      121 TCTGCAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGTC 180

Qy      2266 CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGT 2325
          |||

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Db 181 CAGCTGAATTTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGT 240

Qy 2326 TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTT 2385  
 |||

Db 241 TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTT 300

Qy 2386 TGAATCTGTCATTCACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTAT 2445  
 |||

Db 301 TGAATCTGTCATTCACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTAT 360

Qy 2446 TAAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGTCATCTGTAAAT 2505  
 |||

Db 361 TAAAATCTTCTTCTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGTCATCTGTAAAT 420

Qy 2506 ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT 2565  
 |||

Db 421 ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT 480

Qy 2566 TTACGATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCCTGGTGCAGTGT 2625  
 |||

Db 481 TTACGATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCCTGGTGCAGTGT 540

Qy 2626 CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTC 2685  
 |||

Db 541 CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTC 600

Qy 2686 TAGCATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACA 2745  
 |||

Db 601 TAGCATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACA 660

Qy 2746 TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT 2805  
 |||

Db 661 TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT 720

Qy 2806 AGAAAAGTTTGCTTGACATGGTGCCTTTCTTTTCATCTAGAGGC-AAAAGTCTTTTTGAG 2864  
 |||

Db 721 AGAAAAGTTTGCTTGACATGGTGCCTTTCTTTTCATCTAGAGGC-AAAAGTCTTTTTGAG 780

Qy 2865 ACCGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAG 2924  
 |||

Db 781 ACCGTAAGAACCTCTTACCTTTGTGCGTTCCTGCCTAA-TTTTAAATCTTCTAAGCAAAG 839

Qy 2925 TGCCTTAGGATAGCTTGGG-ATGAGATGTGTGTGAAAGTATGTACAAGAGAA 2975  
 |||

Db 840 TGCCTTAGGATAGCTTGGGAATGAGATGTGTGTGAAAATATGTACAAGAAAA 891

RESULT 11

AL546465

LOCUS AL546465 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL546465 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI030YM19 5-PRIME, mRNA sequence.

ACCESSION AL546465

VERSION AL546465.2 GI:31268299

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1201)
AUTHORS        Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished
COMMENT        On Feb 15, 2001 this sequence version replaced gi:12879606.
                Contact: Genoscope
                Genoscope - Centre National de Sequencage
                BP 191 91006 EVRY cedex - France
                Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                Library was constructed by Life Technologies, a division of
                Invitrogen. This sequence belongs to sequence cluster 7006.r For
                more information about this cluster, see
                http://www.genoscope.cns.fr/
                cgi-bin/cluster.cgi?seq=CS0DI030AG10QP1&cluster=7006.r. Contact :
                Feng Liang Email : fliang@lifetech.com URL :
                http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                Faraday Avenue Genoscope sequence ID : CS0DI030AG10QP1.

FEATURES             Location/Qualifiers
     source            1. .1201
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="CS0DI030YM19"
                        /tissue_type="PLACENTA COT 25-NORMALIZED"
                        /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                        /note="1st strand cDNA was primed with a NotI-oligo(dT)
                        primer. Five prime end enriched, double-strand cDNA was
                        digested with Not I and cloned into the Not I and EcoR V
                        sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT        272 a      289 c      321 g      289 t      30 others
ORIGIN

      Query Match          19.0%;   Score 816.2;   DB 9;   Length 1201;
      Best Local Similarity 97.2%;   Pred. No. 1e-105;
      Matches 854;   Conservative 7;   Mismatches 15;   Indels 3;   Gaps 3;

Qy      178  TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237
          ||      ||
Db      219  TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 278

Qy      238  ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297
          |||||
Db      279  ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 338

Qy      298  CTGTGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357
          |||||
Db      339  CTGTGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 398

Qy      358  CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417
          |||||
Db      399  CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 458

Qy      418  AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477
          |||||
Db      459  AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 518

```

Qy 478 CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537  
 |||  
 Db 519 CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 578  
 Qy 538 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAAGTCC 597  
 |||  
 Db 579 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAAGTCC 638  
 Qy 598 ACACTTCTGAGAATTATCTACAAGAACAGTGCATGCGAAACGGTCCCAATATCTTGATC 657  
 |||  
 Db 639 ACACTTCTGAGAATTATCTACAAGAACAGTGCATGCGAAACGGTCCCAATATCTTGATC 698  
 Qy 658 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 717  
 |||  
 Db 699 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 758  
 Qy 718 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA 777  
 |||  
 Db 759 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA 818  
 Qy 778 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 837  
 |||  
 Db 819 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 878  
 Qy 838 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA 897  
 |||  
 Db 879 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTT-CAAAATGGACAGCAGTA 937  
 Qy 898 GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT 957  
 |||: |||  
 Db 938 GAAATTGTTTTKATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTVTT 997  
 Qy 958 GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT 1017  
 |||: |||: |||  
 Db 998 GATATAATTACGATGGACTACAAAGG-AGTTATCTGCGAATCTGCTTGCTT-MWCCCSGT 1055  
 Qy 1018 CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAA 1056  
 : ||| ||| : |||  
 Db 1056 YARAAGAAAGCTTTCATGCAGTTTTACAAAAMAGCAAAA 1094

RESULT 12

BI858627

LOCUS BI858627 972 bp mRNA linear EST 10-OCT-2001

DEFINITION 603389094F1 NIH\_MGC\_87 Homo sapiens cDNA clone IMAGE:5398054 5', mRNA sequence.

ACCESSION BI858627

VERSION BI858627.1 GI:15999374

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 972)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM12014 row: 1 column: 23  
High quality sequence stop: 899.

FEATURES Location/Qualifiers  
source 1. .972  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5398054"  
/tissue\_type="mammary adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_87"  
/note="Organ: breast; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.383 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

BASE COUNT 230 a 241 c 244 g 256 t 1 others  
ORIGIN

Query Match 18.8%; Score 808.6; DB 12; Length 972;  
Best Local Similarity 96.3%; Pred. No. 1.3e-104;  
Matches 903; Conservative 0; Mismatches 25; Indels 10; Gaps 7;

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Qy      321 GAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCC 380
        |||
Db      1 GAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCC 60

Qy      381 ACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTTCGTTGGCACC 440
        |||
Db      61 ACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTTCGTTGGCACC 120

Qy      441 TGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCC 500
        |||
Db      121 TGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCC 180

Qy      501 CCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTC 560
        |||
Db      181 CCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTC 240

Qy      561 CTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACACTTCTGAGAATTATCTACAA 620
        |||
Db      241 CTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACACTTCTGAGAATTATCTACAA 300

Qy      621 GAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCT 680
        |||
Db      301 GAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCT 360

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Qy 681 GCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC 740  
 |||  
 Db 361 GCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC 420

Qy 741 ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCAC 800  
 |||  
 Db 421 ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCAC 480

Qy 801 TGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAG 860  
 |||  
 Db 481 TGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAG 540

Qy 861 AATTAAAGGAA-TTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGG 919  
 |||  
 Db 541 AATTAAAGGAACTTGGGGTTCCAAAATGGACAGCAGTAGAAATCG-TTTGATTTGGGTGG 599

Qy 920 TCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACA 979  
 |||  
 Db 600 TCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGG-TTTGATATAATTACGATGGACTACA 658

Qy 980 AAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGT 1039  
 |||  
 Db 659 AAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGT 718

Qy 1040 TTTACAAGACAGCAAAAGATTGGT-GGCTGTTTCAGTTTCTATTTCTGCTTGCCATT-GGC 1097  
 |||  
 Db 719 TTTACAAGACAGCAAAAGATTGGTGGGCTATTTCAGTTTCTATTTCTGCTTGCCATNGGGG 778

Qy 1098 CATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCAT 1157  
 |||  
 Db 779 CATCACTGCATTTTTTTTATACACTAATGACCTGTGACATGTTGAGAACGAACAGTGGCTT 838

Qy 1158 GCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTG 1217  
 |||  
 Db 839 GCAGAT--GCTTTAATGATCACCTAAAGCAGAGACGGAA--GTGGCAAAACCGTCTTTG 893

Qy 1218 CCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTC 1255  
 |||  
 Db 894 CCTGGTCCCTGTCTTTGCCCTCTGCTGGGTTCCTTAC 931

# RESULT 13

AL570142/c

LOCUS AL570142 942 bp mRNA linear EST 31-MAY-2003

DEFINITION AL570142 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI005YG20 3-PRIME, mRNA sequence.

ACCESSION AL570142

VERSION AL570142.2 GI:31291568

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 942)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT      On Feb 16, 2001 this sequence version replaced gi:12926160.  
                  Contact: Genoscope  
                  Genoscope - Centre National de Sequencage  
                  BP 191 91006 EVRY cedex - France  
                  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
                  Library was constructed by Life Technologies, a division of  
                  Invitrogen. This sequence belongs to sequence cluster 7006.r For  
                  more information about this cluster, see  
                  http://www.genoscope.cns.fr/  
                  cgi-bin/cluster.cgi?seq=CS0DI005BD10NP1&cluster=7006.r. Contact :  
                  Feng Liang Email : fliang@lifetech.com URL :  
                  http://fulllength.invitrogen.com/ InVitroGen Corporation 1600  
                  Faraday Avenue Genoscope sequence ID : CS0DI005BD10NP1.

FEATURES      Location/Qualifiers  
                  source                    1. .942  
                                             /organism="Homo sapiens"  
                                             /mol\_type="mRNA"  
                                             /db\_xref="taxon:9606"  
                                             /clone="CS0DI005YG20"  
                                             /tissue\_type="PLACENTA COT 25-NORMALIZED"  
                                             /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
                                             /note="1st strand cDNA was primed with a NotI-oligo(dT)  
                                             primer. Five prime end enriched, double-strand cDNA was  
                                             digested with Not I and cloned into the Not I and EcoR V  
                                             sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT      284 a      135 c      152 g      315 t      56 others  
 ORIGIN

Query Match                    18.7%;   Score 802.4;   DB 9;   Length 942;  
 Best Local Similarity        90.0%;   Pred. No. 9.7e-104;  
 Matches 848;   Conservative    54;   Mismatches    34;   Indels        6;   Gaps        5;

```

Qy      2695 TATAATGCTATAGTTAAATACTATTTTTTCAAAATCATACAGA-TTAGTACATTTAACAG 2753
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      942 WAWAAKGCWATAGTTAAAWTRCTATTTTGCAAAATCATRCAGATTTAGWACATTTAACAG 883

Qy      2754 CTACCTGTAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGT 2813
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      882 CTRCCTGTAAAGCTWWTWACTAATTTTTTGTATWATTTTTGTAAATAGCCAATAKAAAAKT 823

Qy      2814 TTGCTTGACATGGTGCCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTTGAGACCGTAAGA 2873
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      822 TTGYTKRACWKGTGCTTTTCTTTCWTCTAGAGGCAAAACTGCTTTTTTGAGACCGTAAGA 763

Qy      2874 ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGG 2933
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      762 RCCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGG 703

Qy      2934 ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAA 2993
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      702 ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAA 643

Qy      2994 TGAGGTGGGGTTGGAGGAAACCCATGGGG-ACAGATTCCCATTCCTTAGCCTAACGTTTCGT 3052
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      642 TGAGGTGGGGTTGGAGGAAACCCATGGGGAACAGATTCCCATTCCTAAGCCTAACGTACGT 583

Qy      3053 CATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAA 3112
  
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      |||
Db      582 CATTGCCTCGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAA 523
Qy      3113 TGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAT 3172
      |||
Db      522 TGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAT 463
Qy      3173 ATGCCCAAATTTTAC--TTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAA 3230
      |||:|:| || |||:| |:|
Db      462 ATGCCCAAATTTTAC--TTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAA 403
Qy      3231 GCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAAC 3290
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      402 GCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACARTAAACCAAAACCCAAC 343
Qy      3291 AATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTA 3350
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      342 AATGTAAMAARAAAAGAAMAAAAAAATWAAATMACACACCAWATGGAAACWATAWA 283
Qy      3351 TAAATCACCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTA 3410
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      282 TAAATCACCACAAACTTAWCCTTVAATTTTCATSCCAATCASTTTBACAGAAGCCTGTAA 223
Qy      3411 TCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCAC 3470
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      222 TCATAGAAGBSATTTTAGACTSTSAATTTTAAATBAATTYTGAATCCCTAATATTTTCAC 163
Qy      3471 AGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTT-TTATTACCATGTACT 3529
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      162 AGTTTATTAATATATTTAATTTCTAATTTTAAATTTTAGATTATTTATTATTACCATGTACT 103
Qy      3530 GAATTTTTCATCCTGATACCCTTTCCTTCTCCATG-TCAGTATCATGTTCTCTAATTAT 3588
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      102 GAATTTTTCATCCWGATACTCTTACCTTCWCCATGATCAGTATCATATTCTCTAATTAT 43
Qy      3589 CTTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCAT 3630
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Db      42 CTTCCCAAATTTTGAAACAACACACAAAAGCATACTGAMAT 1

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# RESULT 14

BU557315

LOCUS BU557315 884 bp mRNA linear EST 16-SEP-2002

DEFINITION AGENCOURT\_10253486 NIH\_MGC\_109 Homo sapiens cDNA clone

IMAGE:6585168 5', mRNA sequence.

ACCESSION BU557315

VERSION BU557315.1 GI:22907611

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 884)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.



Qy	703	CCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAG	762
Db	360	CCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAG	419
Qy	763	CTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTG	822
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Qy	823	AGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCA	882
Db	480	AGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCA	539
Qy	883	AAATGGACAGCAGTAGAAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCT	942
Db	540	AAATGGACAGCAGTAGAAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCT	599
Qy	943	GAAGCCATAGGTTTTTGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGC	1002
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Qy	1003	TTGCTTCATCCCGTTT CAGAAGACAGCTTTTCATGCAGTTTTTCAAGACAGCAAAGATTGG	1062
Db	660	TTGCTTCATCCCGTTT CAGAAGACAGCTTTTCATGCAGTTTTTACCAGACAGCAAAGATTGG	719
Qy	1063	TGGCTGTT CAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTA	1122
Db	720	TGGCTGTT CAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTA	779
Qy	1123	ATGACCTGTGAAATGTT -GAGAAAGAAAAGTGGCATGCAGATTG - -CTTTAAATGATCAC	1179
Db	780	ATGACCTGTGAAATGTTGGAGAAGGAAAAGTGGCATGCCAGATGGCCTTTAAATGATCAC	839
Qy	1180	CTAAAGCAGAGA	1191
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BQ719386

VERSION BQ719386.1 GI:21858283

SOURCE Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT      Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM13603 row: 1 column: 11  
 High quality sequence stop: 606.

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 /note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
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 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.9 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine); available through Life  
 Technologies."

BASE COUNT 273 a 181 c 167 g 289 t 1 others  
 ORIGIN

Query Match 18.4%; Score 792; DB 13; Length 911;  
 Best Local Similarity 95.6%; Pred. No. 2.9e-102;  
 Matches 859; Conservative 0; Mismatches 31; Indels 9; Gaps 4;

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Qy	2430	ATTTTTTCAGGATT	ATTAAATCTTCTTTT	CACTATCGTAGCTTAA	ACTCTGTTTGGT	2489
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Qy	2490	TTTGTCTCTGTAA	ATACTTACCTACATA	CACTGCATGTAGATG	ATTAAATGAGGGCAGG	2549
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Qy	2550	CCCTGTGCTCATAG	CTTTACGATGGAGAG	ATGCCAGTGACCTCATA	ATAAAGACTGTGAA	2609
Db	241	CCCTGTGCTCATAG	CTTTACGATGGAGAG	ATGCCAGTGACCTCATA	ATAAAGACTGTGAA	300
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Db	301	CTGCCTGGTGCAGTGTCCACATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTG	360
Qy	2670	TGGTTAAATGGTTTCTAGCATATGTATAATGCTATAGTTAAATACTATTTTTCAAAT	2729
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Qy	2850	AAACTGCTTTTTGAGACCGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTAT	2909
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Qy	3148	AAGAGCTTTAA---CTCGGTCTTAAATATG---CCCAAATTTTACTTTGTTTTTCT	3199
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